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OM protein - protein search, using sw model

Run on: October 1, 2001, 11:42:49 ; Search time 11.61 Seconds
(without alignments) 563.548 Million cell updates/sec

Title: US-09-479-252-1_COPY_91_281

Perfect score: 996
Sequence: 1 MILRTSEETISTVQEKQONI.....NEHLIDMDHEASFGLVIG 191

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SWISSPROT_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	996	100.0	281	1	TN10_HUMAN
2	693	69.6	291	1	TN10_MOUSE
3	235.5	23.6	316	1	TN11_MOUSE
4	232.5	23.3	317	1	TN11_HUMAN
5	188.5	18.9	279	1	FASL_MOUSE
6	180	18.1	281	1	FASL_HUMAN
7	177.5	17.8	278	1	FASL_RAT
8	152	15.3	260	1	TN14_HUMAN
9	142	14.3	261	1	TN15_BOVIN
10	136.5	13.7	235	1	TN15_BOVIN
11	134.5	13.5	204	1	TN15_RABIT
12	132.5	13.3	234	1	TN15_PIG
13	130	13.1	232	1	TN15_PIG
14	129.5	13.0	235	1	TN15_PIG
15	128.5	12.9	260	1	TN15_MOUSE
16	127.5	12.8	204	1	TN15_BOVIN
17	126	12.7	234	1	TN15_MOUSE
18	125	12.6	233	1	TN15_MOUSE
19	125	12.6	260	1	TN15_FELCA
20	124.5	12.5	261	1	TN15_HUMAN
21	123	12.3	233	1	TN15_HUMAN
22	123	12.3	260	1	TN15_CANFA
23	122.5	12.3	229	1	TN15_CEREL
24	122	12.2	205	1	TN15_HUMAN
25	121	12.1	235	1	TN15_MOUSE
26	121	12.1	235	1	TN15_RAT
27	120	12.0	233	1	TN15_PAPSP
28	117.5	11.8	201	1	TN15_PAPSP
29	117.5	11.8	234	1	TN15_SHEEP
30	117	11.7	233	1	TN15_PAPHU
31	117	11.7	233	1	TN15_PAPHU
32	116.5	11.7	233	1	TN15_CANFA
33	116	11.6	233	1	TN15_MACFA

ALIGNMENTS

RESULT 1	TN10_HUMAN	STANDARD	PRT	281 AA.
AC	P50591			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 10 (TNF-RELATED APOPTOSIS INDUCING LIGAND) (TRAIL PROTEIN) (APO-2 LIGAND) (APO-2L).			
GN	TNFSF10 OR TRAIL OR APO2L.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96111955; Pubmed=8777713;			
RA	Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,			
RA	Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,			
RA	Goodwin R.G.;			
RT	"Identification and characterization of a new member of the TNF family that induces apoptosis."			
RT	Immunoty 3:673-682(1995).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Placenta;			
RC	MEDLINE=96278649; Pubmed=8663110;			
RX	Pitt R.M., Masters S.A., Ruppert S., Donahue C.J., Moore A.,			
RA	Askenazi A.;			
RT	"Induction of apoptosis by Apo-2 ligand, a new member of the tumor necrosis factor cytokine family."			
RT	J. Biol. Chem. 271:12687-12690(1996).			
CC	-1- FUNCTION: INDUCES APOPTOSIS.			
CC	-1- SUBUNIT: HOMOTRIMER (POTENTIAL).			
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).			
CC	-1- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG AND PROSTATE.			
CC	-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.			
CC	-----			
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CC	-----			
CC	EMBL: U37518; AAC50332.1; -			
CC	EMBL: U57059; AAB01233.1; -			
CC	MIM: 603598; -			
CC	InterPro: IPR000478; -			
CC	Pfam: PF00229; TNF_1;			
CC	PROSITE: PS00251; TNF_1; 1.			
CC	PROSITE: PS50045; TNF_2; 1.			
CC	Cytochrome; Transmembrane; Signal-anchor; Apoptosis.			
CC	CYTOLASMIC (POTENTIAL).			
CC	DOMAIN 1 17			

34	114	11.4	202	1	TNFB_MOUSE	P09225	mus musculus
35	113.5	11.4	233	1	TNFA_TRIVU	P79374	trichosurus
36	112	11.2	233	1	TNFA_BOVIN	O06599	bos taurus
37	111.5	11.2	202	1	TNFB_RAT	O06332	rattus norv
38	111	11.1	391	1	EDA_MOUSE	O54693	mus musculus
39	108.5	10.9	306	1	TNFC_MOUSE	P41155	mus musculus
40	108	10.8	193	1	TNFA_CAPIH	P13296	capra hircu
41	108	10.8	233	1	TNFA_MACEU	O77764	macropus eu
42	107	10.7	197	1	TNFB_RABIT	P10154	oryctolagus
43	106	10.6	391	1	EDA_HUMAN	O92838	homo sapien
44	102	10.2	244	1	TNFC_HUMAN	O06643	homo sapien
45	98.5	9.9	233	1	TNFA_FELCA	P19101	felis silve


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RT      to "TRANSC/RAKML.":
RL      Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
RN      [4]
RN      SEQUENCE FROM N.A.
RP      TISSUE=Thymic Lymphoma;
RX      MEDLINE=98032977; PubMed=9367155;
RA      Anderson D.M., Maraskovsky E., Billingsley W.L., Dougal W.C.,
RA      Tomeiko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
RA      Galibert L.;
RT      "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT      and dendritic-cell function.";
RL      Nature 390:175-179(1997).
RN      [5]
RN      SEQUENCE FROM N.A.
RP      Ikeda T.;
RL      Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
CC      ARGUMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
CC      PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS
CC      BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE
CC      REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE..
CC      -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
CC      -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT
CC      NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS
CC      BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE
CC      TRABECULAR BONE AND LUNG.
CC      -1- DISEASE: DECIPHERING IN TNFSF1 RESULTS IN FAILURE TO FORM LOBULO-
CC      ALVEOLAR MAMMARY STRUCTURES DURING PREGNANCY, RESULTING IN DEATH
CC      OF NEONATES. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOPELOSIS, WITH
CC      NO OSTEOCLASTS, MARROW SPACES, OR TOOTH ERUPTION, AND EXHIBIT
CC      PROFOUND GROWTH RETARDATION AT SEVERAL SKELETAL SITES, INCLUDING
CC      THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDROPLASTIA,
CC      WITH THICK, IRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN
CC      HYPERCHROMIC CHONDROCYTES.
CC      -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC      -----
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CC      the European Bioinformatics Institute. There are no restrictions on its
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CC      entities requires a license agreement (See http://www.isb.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF053713; AAC4013.1; -
DR      EMBL; AF013170; AAC7106.1; -
DR      EMBL; AB008426; BAA25425.1; -
DR      EMBL; AF019048; AAB86812.1; -
DR      EMBL; AB036798; BAA97259.1; -
DR      MGD; MGI:1100089; Tnfrsf11.
DR      InterPro; IPR000478; -.
DR      InterPro; IPR003263; -.
DR      Pfam; PF00229; TNF; 1.
DR      ProSite; PS00251; TNF_1; FALSE_NEG.
DR      ProSite; PS50049; TNF_2; 1.
KW      Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW      Signal-anchor.
FT      DOMAIN 1 48 CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM 49 69 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT      FT
FT      DOMAIN 70 316 EXTRACELLULAR (POTENTIAL).
FT      CARBOHYD 197 316 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT      CARBOHYD 262 262 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT      CONFLICT 99 G->D (IN REF. 4).
SO      SEQUENCE 316 AA; 34944 MW; 08DF63A2BE00967A CRC64;

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Dd	107	SEDLTPDSCSRMNOAFGQVQKEIOLHIV-----GPQRSGAPAMMEGSMILDVAQRKPE	160
Qy	34	-----AHTTGRGNSNTLSSNSKNEALGRKINSWSSSSGSEFLSNLHRLNGELYIHEK	89
Dd	161	AQPFNLT-----INAAISIPSGSHKVTL-----SSWYHDR-GNAKISSNMLTNGKRLRVQD	210
Qy	90	GFFYIYSQTFEFCFQEEIKEKTKNDKMOVOYIKRYT-SYDPDLLMKMSANSCMSKDAEYG	148
Dd	211	GFFYLVANICFRHHEISGSPPTDYLDLAMYVKTISKIPSSINMLKKGSTKMSQNSSEFH	270
Qy	149	LYSIYGGIFELKENDRIEVSVTNEHLIDMDHEASEFGAFVY	190
Dd	271	FYSINVGFFFKLRAGEEISIQVSNPSLLDPDOPDAYEFGAFVY	312
RESULT	4		
TN11	HUMAN	STANDARD:	PRT: 317 AA.
ID	TN11_HUMAN	014788: 014723: 09P203;	
AC	01-OCF-2000	(Rel. 40, Created)	
DT	01-OCF-2000	(Rel. 40, Last sequence update)	
DT	01-OCF-2000	(Rel. 40, Last annotation update)	
DE	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 11 (RECEPTOR ACTIVATOR OF NUCLEAR FACTOR KAPPA B LIGAND) (RAKFL) (TNF-RELATED ACTIVATION-INDUCED CYTOKINE) (TRANSC) (OSTEOPROTEGERIN LIGAND) (OPGL) (OSTEOCLAST DIFFERENTIATION FACTOR) (ODF).		
DE	TNFSF11 OR RANKL OR TRANCE OR OPGL.		
GN	Homo sapiens (Human).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxId=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Bone marrow, and Periphereal blood;		
RC	MEDLINE=98032977; PubMed=9367155;		
RX	Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tomelesko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D., Galibert L.;		
RA	"A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function."		
RT	Nature 390:175-179(1997).		
RL	[2]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE=Lymph node;		
RC	MEDLINE=98227661; PubMed=9568710;		
RX	Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H., Sullivan J., Hawkins N., Davy E., Capparello C., Eli A., Qian Y.-X., Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J., Boyle W.J.;		
RA	"Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation."		
RT	Cell 93:165-176(1998).		
RL	[3]		
RN	SEQUENCE OF 73-317 FROM N.A.		
RP	TISSUE=Thymocytes;		
RC	MEDLINE=97460112; PubMed=9312132;		
RX	Wong B.R., Kho Y., Arton J., Rodinson E., Orlinick J., Chao M., Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y., Choi Y.;		
RA	"FRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells."		
RT	J Biol. Chem. 272:25190-25194(1997).		
RL	[4]		
RN	SEQUENCE FROM N.A. (ISOFORM 2).		
RP	TISSUE=Tongue;		
RC	MEDLINE=20175237; PubMed=10708588;		
RX	Nagai M., Kyakumoto S., Sato N.;		
RA	"Cancer cells responsible for humoral hypercalcemia express mRNA encoding a secreted form of ODF/TRANCE that induces osteoclast formation."		
RT	Biochem. Biophys. Res. Commun. 269:532-536(2000).		
CC	-I- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.		

ID	FAST_MOUSE	STANDARD	PRT	279 AA
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	FAS ANTIGEN LIGAND.			
FN	TNFSF6 OR APTILG1 OR FASL OR GLD.			

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090.
RN [1]
RN SEQUENCE FROM N.A. (ISOFORM FASL).
RX RP MEDLINE=94185175; PubMed=7511063;
RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.,
RT "Generalized lymphoproliferative disease in mice, caused by a point
RT mutation in the Fas ligand.";
RT Cell 76:969-976(1994).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RC STRAIN=C57BL/6;
RX RP MEDLINE=95388076; PubMed=7544870;
RA Peitsch M.-J., Tschopp J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
RT of the TNF family.";
RL Mol. Immunol. 32:761-772(1995).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORM FASL).
RX RP MEDLINE=95196085; PubMed=7889405;
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
RT TNF family gene cluster.";
RL Immunity 1:131-136(1994).
RN [4]
RN SEQUENCE FROM N.A. (ISOFORM FASL).
RC STRAIN=BA1B/C;
RA Fenner M.H., Shida T., Isselbacher K.J.;
RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in
RT two amino acids.";
RN Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A. (ISOFORM FASLS).
RC STRAIN=C3H; TISSUE=Spleen;
RX RP MEDLINE=20021694; PubMed=105252956;
RA Ayroldi E., D'Adamo F., Zollo O., Agostini M., Moraca R.,
RA Canmarile L., Migliorati G., Delfino D.V., Riccardi C.;
RT "Cloning and expression of a short Fas ligand: A new alternatively
RT spliced product of the mouse Fas ligand gene.";
RL Blood 94:3456-3467(1999).
RN [6]
RN CHARACTERIZATION OF VARIANT GLD.
RX RP MEDLINE=96091792; PubMed=7495745;
RA Haime M., Peitsch M.C., Immler M., Schroeter M., Lowin B.,
RA Rousseau M., Bron C., Renno T., French L., Tschopp J.;
RT "Characterization of the non-functional Fas ligand of gld mice.";
RL Int. Immunol. 7:1381-1386(1995).
RN [7]
RN FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
RN TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
RN CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
RN FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
RN PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
RN T CELLS, OR BOTH.
RN [8]
RN SUBUNIT: HOMOTRIMER (PROBABLE).
RN [9]
RN SUBCELLULAR LOCATION: ISOFORM FASL IS A TYPE II MEMBRANE PROTEIN.
RN ISOFORM FASLS IS SOLUBLE.
RN [10]
RN ALTERNATIVE PRODUCTS: 2 ISOFORMS; FASL (SHOWN HERE) AND FASLS; ARE
RN PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTOSIS
RN WHILE ISOFORM FASLS PREVENTS APOPTOSIS INDUCED BY FAS/FASL
RN INTERACTION.
RN [11]
RN DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED
RN LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE
RN RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.
RN [12]
RN SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
RN [13]
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	EMBL; U06948;	AAAI7800.1	- ; -	
DR	EMBL; U10984;	AAA19778.1	- ; -	
DR	EMBL; S76752;	AAB33780.1	- ; -	
DR	EMBL; U56995;	AAB02915.1	- ; -	
DR	EMBL; AF119335;	AAD52106.1	- ; -	
DR	HSSP; P01375;	2FNU.		
DR	MCD; MG1:	G9255; Fastl.		
DR	InterPro; IPR000478;	-		
DR	Pfam; PF00228;	TNF_1.		
DR	PROSITE; PS00251;	TNF_1.		
DR	PROSITE; PSS0049;	TNF_2.		
KW	Cycloline; Transmembrane;	Glycoprotein; Signal-anchor; Apoptosis; Cysteine mutation; Alternative splicing. CYTOPLASMIC (POTENTIAL).		
FT	DOMAIN	1 .. 78		
FT	TRANSSEM	79 .. 100		SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN), EXTRACELLULAR (POTENTIAL). PRO-RICH. POLY-PRO. BY SIMILARITY.
FT	DOMAIN	101 .. 279		N-LINKED (GLCNAC..) (POTENTIAL). N-LINKED (GLCNAC..) (POTENTIAL). N-LINKED (GLCNAC..) (POTENTIAL). MISSING (IN ISOFORM FASLUS) . T -> A (IN STRAIN BALB/C) . E -> G (IN STRAIN BALB/C) . F -> L (IN GLD: ABOLISHES BINDING OF FASL TO ITS RECEPTOR) .
FT	DOMAIN	4 .. 69		
FT	DISULFD	200 .. 231		
FT	CARBOHYD	117 .. 117		
FT	CARBOHYD	182 .. 182		
FT	CARBOHYD	248 .. 248-		
FT	CARBOHYD	258 .. 258		
FT	VASSPLIC	1 .. 210		
FT	VARIANT	184 .. 184		
FT	VARIANT	218 .. 218		
FT	VARIANT	273 .. 273		
SEQUENCE	279 AA;	31442 MW;	3797ZEPJ28EOALCA CRC64;	

RESULT	6			
FASL_HUMAN				
ID	FASL_HUMAN	STANDARD:	PRT:	281 AA.
AC	P48023;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APPL).			
CN	TNFSF6 OR APTLIG1 OR FASL.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=95105731; Pubmed=7528780;			
RA	Alderson M.;			

SQ SEQUENCE 281 AA: 31485 MW; A8A6EB358246E9BB CRC64;
 Query Match
 Best Local Similarity 18.1%; Score 180; DB 1; Length 281;
 Matches 54; Conservative 36; Mismatches 66; Indels 40; Gaps 9;
 QY 3 LRTSEETISTVQKQONT---SPLVERGPRVAAHITGTGRSNTLSSPNSKNEKALGR 59
 DB 114 LRETSQMTASLEKQIHPSPP-PEKKELKRVAAHLT---GKSNRSMSP----- 159
 QY 60 KINSWSSSGHSFSLNLRNGELVIEHKGFIYISQTFPRFOEIKENTKNDKQMOVQ 119
 DB 160 --LEWEDT-YGVLLSGVYKKGGLVINEGTFYKSKYFRGQ-----SCNNPLSHK 210
 QY 120 IY-KYTSYDPIILKMSARNS-----CWSKDAEGLYSYOGIPELKNDRIFVSYTN 172
 DB 211 VYMRNRYQDVLMMGKMSYCTTGQMMAR-----SYLGAVNLISADHLVYVNSE 263
 QY 173 EHLIDMDHEASFFGAP 188
 DB 264 LSLVNFESQTEFFGLY 279

RESULT 7

ID FASL_RAT STANDARD: PRT: 278 AA.
 AC P36940;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE FAS ANTIGEN LIGAND.
 GN TNPSF6 OR APTLIG1 OR FASL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1];
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94084792; PubMed=7505205;
 RA Suda T., Takahashi T., Golstein P., Nagata S.;
 RT "Molecular cloning and expression of the Fas ligand, a novel member
 of the tumor necrosis factor family.";
 RL Cell 75:1169-1178(1993).
 CC -1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
 TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
 CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
 CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
 PERIPHERAL TOLERANCE. IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
 T CELLS, OR BOTH.
 CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
 INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
 SURFACE.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND
 THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,
 KIDNEY AND LUNG.
 CC -1- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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 CC -----
 CC EMBL: U03470; AAC52129.1; -
 CC InterPro: IPR000478; -
 CC Pfam: PF00229; TNF_1; 1.
 CC PROSITE: PS00251; TNF_1; 1.
 CC PROSITE: PS50049; TNF_2; 1.
 DR

KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis.
 FT DOMAIN 1 77
 FT TRANSMEM 78 99
 FT DOMAIN 100 278
 FT DOMAIN 100 278
 FT DOMAIN 4 69
 FT DOMAIN 45 58
 FT DISULFID 199 230
 FT CARBOHYD 116 116
 FT CARBOHYD 247 247
 FT CARBOHYD 257 257
 SQ SEQUENCE 278 AA: 31140 MW; 2898E18A862CEAC6 CRC64;
 Query Match
 Best Local Similarity 17.8%; Score 177.5; DB 1; Length 278;
 Matches 50; Conservative 39; Mismatches 64; Indels 29; Gaps 8;

RESULT 8

ID TNF4_HUMAN STANDARD: PRT: 240 AA.
 AC 043557; 075476;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 14 (HERPESVIRUS ENTRY
 MEDIATOR-LIGAND) (HVEM-L).
 GN TNFSF14 OR LIGHT OR HVEM-L.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1];
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98122340; PubMed=9462508;
 RA Mauri D.N., Ebner R., Montgomery R.I., Kochev K.D., Cheung T.C.,
 RA Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,
 RA Ware C.F.;
 RT "LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are
 ligands for herpesvirus entry mediator.";
 RL Immunity 8:21-30(1998).
 CC [2]
 CC SEQUENCE FROM N.A., AND CHARACTERIZATION.
 CC TISSUE=Liver;
 RX MEDLINE=98438532; PubMed=9765287;
 RA Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J.,
 RA Tan K.B., Dede K., Spanpanato J., Silverman C., Hensley P.,
 RA DiPietro R., Emery J.G., Deen K., Elchman C., Chabot-Fletcher M.,
 RA Truneh A., Young P.R.;
 RT "Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for
 RT HVEM/TNFR2, stimulates proliferation of T cells and inhibits HT29 cell
 RT growth.";
 RL J. Biol. Chem. 273:27548-27556(1998).
 CC -1- FUNCTION: ACTIVATES NFkB, STIMULATES THE PROLIFERATION OF T CELLS,
 CC AND INHIBITS GROWTH OF THE ADENOCARCINOMA HT-29. ENGAGES THE
 CC RECEPTOR FOR THE LYMPHOTOXIN-ALPHA-BETA HERPOTRIMER BUT DOES NOT
 CC FORM COMPLEXES WITH EITHER LT-ALPHA OR LT-BETA. ACTS AS A RECEPTOR

CC FOR HERPES SIMPLEX VIRUS.
 CC -1- SUBUNIT: HOMOTRIMER.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
 CC TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE SPLEEN BUT ALSO
 CC FOUND IN THE BRAIN, WEAKLY EXPRESSED IN PERIPHERAL LYMPHOID
 CC TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND KIDNEY,
 CC AND NO EXPRESSION SEEN IN FETAL TISSUES, ENDOCRINE GLANDS, OR
 CC NONHEMATOPOIETIC TUMOR LINES.
 CC -1- INDUCTION: UPREGULATED AFTER T-CELL ACTIVATION.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF036581; AAC39563.1; -
 CC DR EMBL: AF064090; AAC25169.1; -
 CC DR MIR: 604520; -
 CC DR HSSP: P01375; 4TSV.
 CC DR InterPro: IPR000478; -
 CC DR Pfam: PF00229; TNF_1.
 CC DR PROSITE: PS00251; TNF_1; FALSE_NEG.
 CC DR PROSITE: PS50049; TNF_2; 1.
 CC DR Cytochrome; Cytochrome; Transmembrane; Glycoprotein; Signal-anchor.
 CC FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 38 58 EXTRACELLULAR (POTENTIAL).
 CC FT SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
 CC FT (POTENTIAL).
 CC FT DOMAIN 59 240 EXTRACELLULAR (POTENTIAL).
 CC FT CARBOHYD 102 102 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CONFLICT 214 214 E -> K (IN REF. 2).
 CC SQ SEQUENCE 240 AA; 26351 MW; 49D0BF67E1390B39 CRC64;

Query Match 15.3%; Score 152; DB 1; Length 240;
 Best Local Similarity 26.3%; Pred. No. 3.2e-06;
 Matches 50; Conservative 30; Mismatches 56; Indels 54; Gaps 8;

QY 23 LVRRGPGQV-VAHITGRGSRNTLSSPNSKNEKALGRKINSWSSRSGHSLNHLR 80
 DB 83 LIQRSHVPAHILTGANSLSLGSQSP-----LMEF-TQLGLAFLRGLSYH 129
 QY 81 NGELVHEKGYIYISQTYFRPEDEIKENTKNDKQMOY-----IYKYT 124
 DB 130 DQALVTRKAGIYIYISK-----VOLGGVGCPLGLASTITGLYKRT 170
 QY 125 -SYDPTILKMSARNSCMSKDAEYGLY--SIYOGIFELKENDRIEVSVTNEHLIDM-DH 180
 DB 171 PRYEELELVLSQSPGCRATSSSRVMDSSFLGGVHLEAGEEYVAVLDERLRLNDG 230
 QY 181 EASEFGAFLV 190
 DB 231 TRSYGAFAV 240

RESULT 9
 TNFS_BOVIN STANDARD; PRT; 261 AA.
 AC P51749;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CD40 LIGAND (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN
 DE GP39).
 GN TNFSF5 OR CD40LG OR CD40L.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NC NCB1_TaxID=9913;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BLOOD.
 RX MEDLINE=66005582; PubMed=7590981;
 RA Mertens B.E.L.C., Murliki M., Gaidulis L.;
 RT "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
 RT and tumor necrosis factor alpha";
 RL Immunogenetics 42:430-431(1995).
 CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
 CC STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4.
 CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).
 CC -1- SUBUNIT: HOMOTRIMER.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: Z48469; CAAB8363.1; -
 CC DR HSSP: P29965; IALY.
 CC DR InterPro: IPR000478; -
 CC DR Pfam: PF00229; TNF_1.
 CC DR PROSITE: PS00251; TNF_1; 1.
 CC DR PROSITE: PS50049; TNF_2; 1.
 CC DR Cytochrome; Transmembrane; Glycoprotein; Signal-anchor.
 CC FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 23 46 EXTRACELLULAR (POTENTIAL).
 CC FT SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
 CC FT (POTENTIAL).
 CC FT DOMAIN 47 261 EXTRACELLULAR (POTENTIAL).
 CC FT DISULFID 178 218 POTENTIAL.
 CC FT CARBOHYD 240 240 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SQ SEQUENCE 261 AA; 29242 MW; 8491FEFB30A787ED CRC64;

Query Match 14.3%; Score 142; DB 1; Length 261;
 Best Local Similarity 27.7%; Pred. No. 2.6e-05;
 Matches 49; Conservative 33; Mismatches 69; Indels 26; Gaps 8;

QY 13 VQKQONISPLVRRGPGQVVAHITGRGSRNTLSSPNSKNEKALGRKINSWSSRSGH 72
 DB 104 VKKKEKNEHMKGDPEQ-IAAHV-----ISEASSKTSVL-----QW--APKGY 146
 QY 73 FLSN--LHLRNG-ELVHEKGYIYISQTYFRPEDEIKENTKNDKQMOYIYKYTSYDP 129
 DB 147 TLSNNLVLENGKQLAVARQGYIYIYOVTCNSR-----TLQAPFTASLCLSPSGE 202
 QY 130 ILKMSARNSCMSKDAEYGLYSIYOGIFELKENDRIEVSVTNEHLIDMDEASFFG 186
 DB 203 RILRAANTHSSSKPC--GQOSIHGVEFELGASVAVNTDPSVSHGTFSTFG 257

RESULT 10
 TNFA_RABBIT STANDARD; PRT; 235 AA.
 AC P04924;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
 GN TNF OR TNFA.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NC NCB1_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91065534; PubMed=2249779;

RA	Shakhov A.N., Kuprash D.V., Azizov M.M., Jongeneel C.V.,	CC	
RA	Nedospasov S.A.;	CC	
RT	"Structural analysis of the rabbit TNF locus, containing the genes	CC	
RT	encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis	CC	
RT	factor).";	CC	
RL	Gene 95:215-221(1990).	CC	
RL	[12]	CC	
RN	SEQUENCE FROM N.A.	CC	
RP	MEDLINE-86219712; PubMed-3519138;	CC	
RX	Ito H., Yamamoto S., Kuroda S., Sakamoto H., Kajihara J., Kiyota T.,	CC	
RA	Wallace R.B.;	CC	
RT	"Molecular cloning of the gene encoding rabbit tumor necrosis	CC	
RT	factor.";	CC	
RL	DNA 5:157-165(1986).	CC	
RL	[13]	CC	
RP	SEQUENCE FROM N.A.	CC	
RX	MEDLINE-86219711; PubMed-3519137;	CC	
RA	Ito H., Yamamoto S., Kuroda S., Sakamoto H., Kajihara J., Kiyota T.,	CC	
RA	Hayashi H., Kato M., Sako M.;	CC	
RT	"Molecular cloning and expression in Escherichia coli of the cDNA	CC	
RT	coding for rabbit tumor necrosis factor.";	CC	
RL	DNA 5:149-156(1986).	CC	
CC	-1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE	CC	
CC	WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF	CC	
CC	CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF	CC	
CC	CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION	CC	
CC	OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE	CC	
CC	CELL DIFFERENTIATION AND INDUCE CELL DEREGULATION UNDER CERTAIN	CC	
CC	CONDITIONS.	CC	
CC	-1- SUBUNIT: HOMOTRIMER.	CC	
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN	CC	
CC	EXTRACELLULAR SOLUBLE FORM.	CC	
CC	-1- PM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY	CC	
CC	PROTEOLYTIC PROCESSING.	CC	
CC	-1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING	CC	
CC	CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH	CC	
CC	AND MALNUTRITION.	CC	
CC	-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	CC	
CC	-----	CC	
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	CC	
CC	or send an email to license@isb-sib.ch).	CC	
CC	-----	CC	
DR	EMBL, M12845; AAA31486.1; -;	CC	
DR	EMBL, M12846; AAA31482.1; -;	CC	
DR	EMBL, M60340; AAA31484.1; -;	CC	
DR	PIR; A25451; A25451.	CC	
DR	PIR; A25454; A25454.	CC	
DR	PIR; J50727; J50727.	CC	
DR	HSP, P01375; TNF.	CC	
DR	InterPro; IPR000478; -;	CC	
DR	InterPro; IPR002959; -;	CC	
DR	Pfam; PF00229; TNF; 1.	CC	
DR	PRINTS; PRO1234; TNCRSISFCT.	CC	
DR	PRINTS; PRO1235; TNCRSISFCT.	CC	
DR	PROSITE; PS00251; TNF_1; 1.	CC	
DR	PROSITE; PS00049; TNF_2; 1.	CC	
KW	Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.	CC	
FT	PROPEP 1 79	CC	
FT	CHAIN 80 235	CC	
FT	TRANSMEM 36 56	CC	
FT	DISULFID 148 179	CC	
FT	CONFLICT 63 63	CC	
FT	SEQUENCE 235 AA; 25816 MW; 610177DD0BDE5F71 CRC64;	CC	

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0Y  ISPLVREGGPQVAAHIIGTGRSNTL--SPNSXKNEALGKINS-----WESSRG 70
Db  IGPQEEBSPNNL--HLVNPVAQMVTLLRSASRLSDKPLAHVAVNPQEGOLOMLSORAN 113
0Y  71 HSPFLNLRLNGELVIEHKGFFYYYSQTYFFRQFEIKENTKNDQOMVOYLKY--TSYDP 129
Db  114 ALLANGMKLTJNGLVLRPADGILYLLYSQVLESGQ-----GCSYVLLHVTYSRFAVSTPK 168
0Y  130 ILLMKARNCSWCKDAEYG-----LYSYOGGIFELKENDRIEVSVTNEHLIDMDHEAS- 183
Db  169 VNLISAIKSPCHRETPDEAEAPMAWYERPIYLGVPQLKEDRLSTEVNQPELDLAESGV 228
0Y  184 FFG 186
Db  229 YFG 231

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AC	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AV	AW	AX	AY	AZ	BA	BB	BC	BD	BE	BF	BG	BH	BI	BJ	BK	BL	BM	BN	BO	BP	BQ	BR	BS	BT	BV	BW	BX	BY	BZ	CA	CB	CC	CD	CE	CF	CG	CH	CI	CJ	CK	CL	CM	CN	CO	CP	CQ	CR	CS	CT	CU	CV	CW	CX	CY	CZ	DA	DB	DC	DD	DE	DF	DG	DH	DI	DJ	DK	DL	DM	DN	DO	DP	DQ	DR	DS	DT	DU	DV	DW	DX	DY	DZ	EA	EB	EC	ED	EE	EF	EG	EH	EI	EJ	EK	EL	EM	EN	EO	EP	EQ	ER	ES	ET	EU	EV	EW	EX	EY	EZ	FA	FB	FC	FD	FE	FF	FG	FH	FI	FJ	FK	FL	FM	FN	FO	FP	FQ	FR	FS	FT	FU	FV	FW	FX	FY	FZ	GA	GB	GC	GD	GE	GF	GG	GH	GI	GJ	GK	GL	GM	GN	GO	GP	GQ	GR	GS	GT	GU	GV	GW	GX	GY	GZ	HA	HB	HC	HD	HE	HF	HG	HH	HI	HJ	HK	HL	HM	HN	HO	HP	HQ	HR	HS	HT	HU	HV	HW	HX	HY	HZ	IA	IB	IC	ID	IE	IF	IG	IH	II	IJ	IK	IL	IM	IN	IO	IP	IQ	IR	IS	IT	IU	IV	IW	IX	IY	IZ	JA	JB	JC	JD	JE	JF	JG	JH	JI	JJ	JK	JL	JM	JN	JO	JP	JQ	JR	JS	JT	JU	JV	JW	JX	JY	JZ	KA	KB	KC	KD	KE	KF	KG	KH	KI	KJ	KK	KL	KM	KN	KO	KP	KQ	KR	KS	KT	KU	KV	KW	KX	KY	KZ	LA	LB	LC	LD	LE	LF	LG	LH	LI	LJ	LK	LL	LM	LN	LO	LP	LQ	LR	LS	LT	LU	LV	LW	LX	LY	LZ	MA	MB	MC	MD	ME	MF	MG	MH	MI	MJ	MK	ML	MM	MN	MO	MP	MQ	MR	MS	MT	MU	MV	MW	MX	MY	MZ	NA	NB	NC	ND	NE	NF	NG	NH	NI	NJ	NK	NL	NM	NO	NP	NQ	NR	NS	NT	NU	NV	NW	NX	NY	NZ	OA	OB	OC	OD	OE	OF	OG	OH	OI	OJ	OK	OL	OM	ON	OO	OP	OQ	OR	OS	OT	OU	OV	OW	OX	OY	OZ	PA	PB	PC	PD	PE	PF	PG	PH	PI	PJ	PK	PL	PM	PN	PO	PP	PQ	PR	PS	PT	PV	PW	PX	PY	PZ	QA	QB	QC	QD	QE	QF	QG	QH	QI	QJ	QK	QL	QM	QN	QO	QP	QQ	QR	QS	QT	QU	QV	QW	QX	QY	QZ	RA	RB	RC	RD	RE	RF	RG	RH	RI	RJ	RK	RL	RM	RN	RO	RP	RQ	RR	RS	RT	RU	RV	RW	RX	RY	RZ	SA	SB	SC	SD	SE	SF	SG	SH	SI	SJ	SK	SL	SM	SN	SO	SP	SQ	SR	SS	ST	SU	SV	SW	SX	SY	SZ	TA	TB	TC	TD	TE	TF	TG	TH	TI	TJ	TK	TL	TM	TN	TO	TP	TQ	TR	TS	TT	TU	TV	TW	TX	TY	TZ	UA	UB	UC	UD	UE	UF	UG	UH	UI	UJ	UK	UL	UM	UN	UO	UP	UQ	UR	US	UT	UU	UV	UW	UX	UY	UZ	VA	VB	VC	VD	VE	VF	VG	VH	VI	VJ	VK	VL	VM	VN	VO	VP	VQ	VR	VS	VT	VU	VV	VX	VY	VZ	WA	WB	WC	WD	WE	WF	WG	WH	WI	WJ	WK	WL	WM	WN	WO	WP	WQ	WR	WS	WT	WU	WV	WW	WX	WY	WZ	XA	XB	XC	XD	XE	XF	XG	XH	XI	XJ	XK	XL	XM	XN	XO	XP	XQ	XR	XS	XT	XU	XV	XW	XX	XY	XZ	YA	YB	YC	YD	YE	YF	YG	YH	YI	YJ	YK	YL	YM	YN	YO	YP	YQ	YR	YS	YT	YU	YV	YW	YX	YZ	ZA	ZB	ZC	ZD	ZE	ZF	ZG	ZH	ZI	ZJ	ZK	ZL	ZM	ZN	ZO	ZP	ZQ	ZR	ZS	ZT	ZU	ZV	ZW	ZX	ZY	ZZ	AA	AB	AC	AD	AE	AF	AG
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Query Match	13.7%;	Score 136.5;	DB 1;	Length 235;
Best Local Similarity	23.0%;	Pred. No. 6.7e-05;		
Matches	42;	Conservative 37;	Mismatches 81;	Indels 23; Gaps 7;

Query Match	13.5%;	Score 134.5;	DB 1;	Length 204;
Best Local Similarity	24.7%;	Pred. No. 8.3e-05;		
Matches 46;	Conservative 31;	Mismatches 76;	Indels 33;	Gaps 7


```
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: X54001; CAA37949.1; -
CC EMBL: X54859; CAA38639.1; -
CC EMBL: X57321; CAA40591.1; -
CC EMBL: M29079; AAA31128.1; -
CC PIR: S12606; S12606.
CC PIR: S17290; S17280.
CC PIR: S18965; S18965.
CC HSSP: P01375; 2TUN.
CC InterPro: IPR000478; -
CC InterPro: IPR002959; -
CC Pfam: PF00229; TNF_1.
CC PRINTS: PRO1234; TNFCROSISFCT.
CC PRINTS: PRO1235; TNFALPHA.
CC PROSITE: PS00251; TNF_1; 1.
CC PROSITE: PS50049; TNF_2; 1.
CC Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
CC PROPEP 1 76
CC CHAIN 77 232 TUMOR NECROSIS FACTOR.
CC TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
CC DISULFID 144 176 BY SIMILARITY.
CC SEQUENCE 232 AA; 25254 MW; 65B28F702D99C8BE CRC64;

Query Match 13.1%; Score 130; DB 1; Length 232;
Best Local Similarity 25.1%; Pred. No. 0.00024;
Matches 43; Conservative 30; Mismatches 78; Indels 20; Gaps 6;

QY 28 GQRYVAHHTGTRGRSNTLTSSPNS--KNEKALGRKINSWESSRSGHSFLSNLHNGEL 84
DB 66 GPLSINPLAAGLRSSQTSQDKPAHVAVANKAGQL--QWOSYAAALLANGKAKLDNQL 123
QY 85 VHKGFYIYISQTYFRQEEIKEN--TKNDKQWQYIYKYTSYDPILMKASNSCM 141
DB 124 VPTDGLIYIYSQVLEFRGCGPSTNFWLTHITISRIA-----VSYOTKVLMLSAIKSPQC 177
QY 142 SK-----DAEYGLYSYOGGIFELKENDRIEFSVTNEHLIDMHENS-FFG 186
DB 178 REPPEGAEKAPWEPIYILGVFQLEKDRLSAEINLPDYLDFAESGQVYFG 228

RESULT 14
TNFA_PERLE STANDARD: PRT: 235 AA.
AC P36939;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNF OR TNFA.
```

```
OS Peromyscus leucopus (white-footed mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10041;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92218012; PubMed=1348497;
RA Crew M.D., Filipowsky M.E.;
RT "Sequence of the tumor necrosis factor/cachectin (TNF) gene from
RT Peromyscus leucopus (family Cricetidae).";
RL Immunogenetics 35:351-353(1992).
CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: M59233; AAA0596.1; -
CC HSSP: P01375; 2TUN.
CC InterPro: IPR000478; -
CC InterPro: IPR002959; -
CC Pfam: PF00229; TNF_1.
CC PRINTS: PRO1234; TNFCROSISFCT.
CC PRINTS: PRO1235; TNFALPHA.
CC PROSITE: PS00251; TNF_1; 1.
CC PROSITE: PS50049; TNF_2; 1.
CC Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
CC PROPEP 1 79
CC CHAIN 80 235 TUMOR NECROSIS FACTOR.
CC TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
CC DISULFID 148 179 BY SIMILARITY.
CC CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 235 AA; 25822 MW; 235A5CFC9F9AC624 CRC64;

Query Match 13.0%; Score 129.5; DB 1; Length 235;
Best Local Similarity 24.5%; Pred. No. 0.00027;
Matches 45; Conservative 39; Mismatches 75; Indels 25; Gaps 9;

QY 20 ISPLVERGQRYVAHHTGTRGRSNTLTSSPNSKNEKALGRKINSW-----SSRSCH 71
DB 56 IGQREKEPPNNLP--ITGSMQTLTLRSSQSSQDKPAHVAVANQVDEQLEWLSRGAN 113
QY 72 SFLSN-LHLRNGELVHEKGFYIYISQTYFRQEEIKENTKNDKQWQYIYKY-TSYPP 129
DB 114 ALLANGMDLKDNQVLPAGGLVYISQVLEFKG-----GCSSVLLTHVSRRAVSYEOK 168
QY 130 IILMKASNSCWSKDAEY-----LYSIYOGGIFELKENDRIEFSVTNEHLIDMHENS 183
DB 169 VNLSAIKSPC-PKEPPESEILKPYEPIYILGVFQLEKDRLSAEVNPKYDFAESQ 227
QY 184 -FFG 186
:11
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Db 228 VFEG 231

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RESULT 15
TNFS_MOUSE STANDARD; PRT; 260 AA.
AC P27548;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE CD40 LIGAND (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN
DE GP39).
GN TNFSF5 OR CD40LG OR CD40L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI:TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9224364; Pubmed=1374165;
RA Armitage R., Fanslow W., Sato T.A., Clifford K.N., Shrockbine L.,
RA Macduff B.M., Anderson D.M., Gimpe J.S.D., Davis-Smith T.,
RA Maliszewski C.R., Clark E.A., Smith C.A., Grabstein K.H., Cosman D.,
RA Spriggs M.K.;
RT "Molecular and biological characterization of a murine ligand for
RT CD40."
RL Nature 357:80-82(1992).
RN [2]
RP SIMILARITY TO THE TNF FAMILY.
RX MEDLINE=92310561; Pubmed=1377364;
RA Farrah T., Smith C.A.;
RT "Emerging cytokine family."
RL Nature 358:26-26(1992).
RN [3]
RP 3D-STRUCTURE MODELING OF 115-260.
RX MEDLINE=9320072; Pubmed=8095800;
RA Peltch M.C., Jongeneel C.V.;
RT "A 3-D model for the CD40 ligand predicts that it is a compact trimer
RT similar to the tumor necrosis factors."
RL Int. Immunol. 5:233-238(1993).
CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
CC STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4.
CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+
CC T-LYMPHOCYTES.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X65453; CAA46448.1; -.
DR PIR: S21738; S21738.
DR PDB: 1CDA; 31-OCT-93.
DR MGD: MGI:88337; Tnfsf5.
DR InterPro: IPR000478; -.
DR Pfam: PF00228; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
KM Cytokine; Transmembrane; Glycoprotein; Signal-anchor; 3D-structure.
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL)
FT TRANSMEM 23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT 47 260 (POTENTIAL)
FT DISULFID 177 217 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).

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SQ SEQUENCE 260 AA; 29396 MW; 7E0F34F7473668B7 CRC64;

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Query Match 12.9%; Score 128.5; DB 1; Length 260;
Best Local Similarity 25.3%; Pred. No. 0.00037;
Matches 44; Conservative 35; Mismatches 68; Indels 27; Gaps 8;

QY 4 RTSETISTV---OEKOONISPLVRENGPQVAHITGTRGRNTLTSSPSKNEKALGR 59
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 89 RQFEDLVADITLKNKEKNSFEKQDEDEPQIAHV-----VSEANSMAASVL- 137
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 KINSMESSRSCHSFLSNL-HLRNG-ELVIHEKGFYIYSQTFPFOEIKENFTKNDKQMV 117
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 138 ---QW-AKKGYITMKSNTVMLENGKQLVKKREGLYVYTVQTFCSNRE---PSSQRFI 189
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 118 QYIKYYSYPPDILMKSARNSCSKDAEYGLYSIYOGGIFELKENDRIEVSVT 171
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 190 VGLMLKPSIGSERILKKAANTHSSSOICEQ--QSVHLGVEFELQAGASVFVNVT 241
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: October 1, 2001, 11:44:41
 Job time: 112 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 1, 2001, 11:41:44 ; Search time 12.27 Seconds
(without alignments)
320.518 Million cell updates/sec

Title: US-09-479-252-1_COPY_91_281

Perfect score: 996
Sequence: 1 MILRTSEETISIVGEKQNI.....NEHLIDMDHEASFGAFELVG 191

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

fred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	996	100.0	281	1 US-08-670-354-2	Sequence 2, Appl
2	996	100.0	281	3 US-08-584-031-1	Sequence 1, Appl
3	996	100.0	281	3 US-08-780-496-1	Sequence 1, Appl
4	996	100.0	281	4 US-08-883-086-10	Sequence 10, Appl
5	996	100.0	281	5 PCT-US96-10895-2	Sequence 7, Appl
6	930	93.4	177	1 US-09-105-343A-7	Sequence 7, Appl
7	693	69.6	291	1 US-08-670-354-6	Sequence 6, Appl
8	693	69.6	291	5 PCT-US96-10895-6	Sequence 6, Appl
9	654	65.7	183	4 US-09-105-343A-8	Sequence 8, Appl
10	235.5	23.6	294	4 US-08-996-139-11	Sequence 11, Appl
11	235.5	23.6	316	2 US-08-995-659-11	Sequence 11, Appl
12	235.5	23.6	316	4 US-08-842-842-7	Sequence 7, Appl
13	235.5	23.6	316	4 US-08-969-362-2	Sequence 2, Appl
14	232.5	23.3	317	3 US-08-996-139-13	Sequence 13, Appl
15	232.5	23.3	317	4 US-08-995-659-13	Sequence 13, Appl
16	184.5	18.5	279	5 PCT-US95-00362-5	Sequence 9, Appl
17	180	18.1	281	3 US-08-649-100-9	Sequence 9, Appl
18	180	18.1	281	2 US-08-810-453-2	Sequence 2, Appl
19	180	18.1	281	3 US-08-815-190A-2	Sequence 2, Appl
20	180	18.1	281	4 US-09-290-640-25	Sequence 25, Appl
21	180	18.1	281	4 US-09-479-524-3	Sequence 3, Appl
22	180	18.1	281	5 PCT-US95-00362-2	Sequence 2, Appl
23	180	18.1	287	3 US-08-815-190A-16	Sequence 16, Appl
24	178	17.9	145	3 US-08-630-172-5	Sequence 5, Appl
25	178	17.9	376	3 US-08-751-512-8	Sequence 8, Appl
26	178	17.9	378	3 US-08-630-172-21	Sequence 21, Appl
27	175.5	17.6	149	3 US-08-584-031-17	Sequence 17, Appl

28	154	15.5	240	4 US-08-913-014A-1	Sequence 1, Appl
29	152.5	15.3	239	4 US-08-913-014A-2	Sequence 2, Appl
30	147.5	14.8	239	4 US-08-913-014A-3	Sequence 3, Appl
31	130	13.1	170	6 5180811-11	Patent No. 5180811
32	130	13.1	187	6 5180811-13	Patent No. 5180811
33	128.5	12.9	260	2 US-08-431-055-2	Sequence 2, Appl
34	127.5	12.8	171	5 PCT-US93-02475-11	Sequence 11, Appl
35	127.5	12.8	260	1 US-08-446-922-6	Sequence 6, Appl
36	127.5	12.8	260	2 US-08-249-189-2	Sequence 2, Appl
37	127.5	12.8	260	2 US-08-484-624A-2	Sequence 2, Appl
38	127.5	12.8	260	2 US-08-477-733B-2	Sequence 2, Appl
39	127.5	12.8	260	3 US-09-088-913A-2	Sequence 2, Appl
40	127.5	12.8	260	5 PCT-US93-10034-6	Sequence 6, Appl
41	127.5	12.8	280	2 US-08-249-189-23	Sequence 23, Appl
42	127.5	12.8	280	2 US-08-484-624A-23	Sequence 23, Appl
43	127.5	12.8	280	2 US-08-477-733B-23	Sequence 23, Appl
44	127.5	12.8	280	3 US-09-088-913A-23	Sequence 23, Appl
45	125.5	12.6	161	1 US-07-994-469A-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1
US-08-670-354-2
: Sequence 2, Application US/08670354
: Patent No. 5763223
: GENERAL INFORMATION:
: APPLICANT: Steven R. Wiley and
: APPLICANT: Raymond G. Goodwin.
: TITLE OF INVENTION: Cytokine That Induces Apoptosis
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Apple 7.5.2
: SOFTWARE: Microsoft Word, Version 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/670,354
: FILING DATE: 25-JUN-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/496,632
: FILING DATE: 29-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/548,368
: FILING DATE: 01-NOV-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Anderson, Kathryn A.
: REGISTRATION NUMBER: 32,172
: REFERENCE/DOCKET NUMBER: 2835-B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 587-0430
: TELEFAX: (206) 233-0644
: TELEX: 756822
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 281 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-670-354-2

	Query Match	100.0%;	Score	996;	D8	1	Length	281;		
	Best Local Similarity	100.0%;	Pred. No.	3	88	98;				
	Matches	191;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Oy	1	MILRTSEETISTVQEKQONISPLVBERGPQVAAHITGRGSNTLSSPNSKNEKALGRK	60							
Db	91	MILRFSEETISTVQEKQONISPLVBERGPQVAAHITGRGSNTLSSPNSKNEKALGRK	150							
Oy	61	INSWSSRSRGSHFSLNLHLRNGELVIHKEGFIYYSQTFRRROEIKENTKDKQWQYI	120							
Db	151	INSWSSRSRGSHFSLNLHLRNGELVIHKEGFIYYSQTFRRROEIKENTKDKQWQYI	210							
Oy	121	YKYTYSPPDILMLKARNSCWSKDAEYGLYSITYGIFELKENDRIFVSVTNEHLIDMH	180							
Db	211	YKYTYSPPDILMLKARNSCWSKDAEYGLYSITYGIFELKENDRIFVSVTNEHLIDMH	270							
Oy	181	EASFEGAFVNG	191							
Db	271	EASFEGAFVNG	281							

```

US-08-584-031-1
:
: Sequence 1, Application US/08584031A
: Patent No. 6030945
:
: GENERAL INFORMATION:
:
: APPLICANT: Ashkenazi, Avi J.
: TITLE OF INVENTION: APO-2 LIGAND
: FILE REFERENCE: 11669.2,210503
: CURRENT APPLICATION NUMBER: US/08/584,031A
: CURRENT FILING DATE: 1996-01-09
: NUMBER OF SEQ ID NOS: 17
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 1
:
: LENGTH: 281
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
:
: US-08-584-031-1

```

Query Match	100.0%	Score	996	DB 3	Length	281			
Best Local Similarity	100.0%	Pred. No.	3	8e-98					
Matches	191	Conservative	0	Mismatches	0	Indels	0	Gaps	0
QY	1	MILRTSEETISTVQEKQOONISPLVBERGDPVAAAHITGRGSNTLSPDSENKALGRK	60						
Db	91	MILRFSEETISTVQEKQOONISPLVBERGDPVAAAHITGRGSNTLSPDSENKALGRK	150						
QY	61	INSMSSSGSHSEFNLRLNGELVTHEKGYYIYSQYFRQEEFKETKNDKQWQYI	120						
Db	151	INSMSSSGSHSEFNLRLNGELVTHEKGYYIYSQYFRQEEFKETKNDKQWQYI	210						
QY	121	YKYSYSPPIILMKARSNCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDH	180						
Db	211	YKYSYSPPIILMKARSNCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDH	270						
QY	181	EASFPGAFVLG	191						
Db	271	EASFPGAFVLG	281						

RESULT 3
US-08-780-496-1
Sequence 1, Application US/08780496
Patent No. 6046048
GENERAL INFORMATION:
APPLICANT: AVI Ashkenazi, Anan Chunchatrapai, Kyung Jin Kim
TITLE OF INVENTION: Apo-2 Ligand
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco

```

1  STATE: California
2
3  COUNTRY: USA
4
5  ZIP: 94080
6
7  COMPUTER READABLE FORM:
8
9  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
10
11  COMPUTER: IBM PC compatible
12
13  OPERATING SYSTEM: PC-DOS/MS-DOS
14
15  SOFTWARE: Winpatlin (Genentech)
16
17  CURRENT APPLICATION DATA:
18
19  APPLICATION NUMBER: US/08/780,496
20
21  FILING DATE: 08-Jan-1997
22
23  CLASSIFICATION: 435
24
25  ATTORNEY/AGENT INFORMATION:
26
27  NAME: Mairschang, Diane L.
28
29  REGISTRATION NUMBER: 35,600
30
31  REFERENCE/DOCKET NUMBER: P0978P1
32
33  TELECOMMUNICATION INFORMATION:
34
35  TELEPHONE: 415/225-5416
36
37  TELEFAX: 415/952-9881
38
39  TELE: 910/371-7168
40
41  INFORMATION FOR SEQ ID NO: 1:
42
43  SEQUENCE CHARACTERISTICS:
44
45  LENGTH: 281 amino acids
46
47  TYPE: Amino acid
48
49  TOPOLOGY: Linear
50
51  US-08-780-496-1

```

Query Match	100.0%;	Score 996;	DB 3;	Length 281;
Best Local Similarity	100.0%;	Pred. No. 3.8e-98;		
Matches 191;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	MILRSEETISTVOEKÖONISPLVREKRPQVAHINTGRSRWTSSPSNKALGR	60
Db	91	MILRSEETISTVOEKÖONISPLVREKRPQVAHINTGRSRWTSSPSNKALGR	150
Qy	61	INSWESSRSGHSFLSNLHRLNGELVHEKGFYYISQYFRFOEIKENTKNDKÖWÖYI	120
Db	151	INSWESSRSGHSFLSNLHRLNGELVHEKGFYYISQYFRFOEIKENTKNDKÖWÖYI	210
Qy	121	YKYSYSPDPIILMKSARNSCSKAEBGLSITYOGIFELKENDRIVSVTNEHLDMDH	180
Db	211	YKYSYSPDPIILMKSARNSCSKAEBGLSITYOGIFELKENDRIVSVTNEHLDMDH	270
Qy	181	EASFEGAFVLG 191	
Db	271	EASFEGAFVLG 281	

RESULT 4
US-08-883-086-10
Sequence 10, Application us/08883086
Patent No. 6171787
GENERAL INFORMATION:
APPLICANT: WILEY, STEVEN
TITLE OF INVENTION: MEMBER OF THE FAMILY USEFUL
TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 2.0
CURRENT APPLICATION DATA: US/08/883.086
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6134, US, 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-0378
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6171787e
US-08-883-086-10

Query Match 100.0%; Score 996; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MILRTSEETISTVOEKQONISPLVREKGPQVAAHITGRGRSMTLSSPNSKNEKALGRK 60
DB 91 MILRTSEETISTVOEKQONISPLVREKGPQVAAHITGRGRSMTLSSPNSKNEKALGRK 150
QY 61 INSNESSRSGHSFLSNLHRLNGELVHHEKGFYIYSQTYFFRFOEIKENTNDKQMOYI 120
DB 151 INSNESSRSGHSFLSNLHRLNGELVHHEKGFYIYSQTYFFRFOEIKENTNDKQMOYI 210
QY 121 YKITSYDPILMKSARNSCKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDH 180
DB 211 YKITSYDPILMKSARNSCKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDH 270
QY 181 EASFFGAFVWG 191
DB 271 EASFFGAFVWG 281

RESULT 5
PCT-US96-10895-2
Sequence 2, Application PC/TUS9610895
GENERAL INFORMATION:
APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10895-2

Query Match 100.0%; Score 996; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MILRTSEETISTVOEKQONISPLVREKGPQVAAHITGRGRSMTLSSPNSKNEKALGRK 60
DB 91 MILRTSEETISTVOEKQONISPLVREKGPQVAAHITGRGRSMTLSSPNSKNEKALGRK 150
QY 61 INSNESSRSGHSFLSNLHRLNGELVHHEKGFYIYSQTYFFRFOEIKENTNDKQMOYI 120
DB 151 INSNESSRSGHSFLSNLHRLNGELVHHEKGFYIYSQTYFFRFOEIKENTNDKQMOYI 210
QY 121 YKITSYDPILMKSARNSCKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDH 180
DB 211 YKITSYDPILMKSARNSCKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDH 270
QY 181 EASFFGAFVWG 191
DB 271 EASFFGAFVWG 281

RESULT 6
US-09-105-343A-7
Sequence 7, Application US/09105343A
Patent No. 6207642
GENERAL INFORMATION:
APPLICANT: WILEY, S.R.
TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
FOR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-6050
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Fastseq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,343A
FILING DATE: 12-FEB-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/02859
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: BECKER, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6048, US, P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-935-1729

```

:
:
:
: TELEFAX: 847-938-2623
:
:
:
:
: TELE:
:
:
: INFORMATION FOR SEQ ID NO: 7:
:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 177 amino acids
:
: TYPE: amino acid
:
: STRANDEDNESS: single
:
: TOPOLOGY: linear
:
:
: MOLECULE TYPE: NO. 6207642e
:
:
: OS-09-105-343A-7

```

Query Match	93.4%	Score 930:	DB 4:	Length 177:
Best Local Similarity	99.4%	Pred. No. 2.1e-91:		
Matches 176; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0

Qy	15	EKOONISPLVYERGCORAAAHITOTRGNSNLTSSPSNKNENKALGRKINWESSNUGHSFL	74
Db	1	EKOONISPLVYERGCORAAAHITOTRGNSNLTSSPSNKNENKALGRKINWESSNUGHSFL	60
Qy	75	SNLHNRNELVTHEHGEFYIISQTFYFRROEIKRNTKNDKQMOYIYKYTSYPPILLMK	134
Db	61	SNLHNRNELVTHEHGEFYIISQTFYFRROEIKRNTKNDKQMOYIYKYTSYPPILLMK	120
Qy	135	SARNSCWAKDEYGLIYSGIGITELKENDRIEVSYNHEHLIDMDHASFAGIAVLG	191
Db	121	SARNSCWAKDEYGLIYSGIGITELKENDRIEVSYNHEHLIDMDHASFAGIAVLG	177

US-08-670-354-6
 Sequence 6, Application US/08670354
 Patent No. 5763223
 GENERAL INFORMATION:
 APPLICANT: Steven R. Wiley and
 APPLICANT: Raymond G. Goodwin.
 TITLE OF INVENTION: Cytokine That Induces Apoptosis
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple 7.5.2
 SOFTWARE: Microsoft Word, Version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/670.354
 FILING DATE: 25-JUN-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/496,632
 FILING DATE: 29-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/548,368
 FILING DATE: 01-NOV-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Anderson, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2835-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEX: 756822
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 291 amino acids

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;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-670-354-6

```

Query Match	69.6%;	Score 693;	DB 1;	Length 291;
Best Local Similarity	69.1%;	Pred. No. 6.8e-66;		
Matches 134;	Conservative 23;	Mismatches 31;	Indels 6;	Gaps 1

[illegible]

RESULT 8
 PCT-US96-10895-6
 Sequence 6, Application PC/TUS9610895
 GENERAL INFORMATION:
 APPLICANT: Immunex Corporation.
 TITLE OF INVENTION: Cytokine That Induces Apoptosis
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple 7.5.2
 SOFTWARE: Microsoft Word, Version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/10895
 FILING DATE: 25-JUN-1996
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/496,632
 FILING DATE: 29-JUN-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/548,368
 FILING DATE: 01-NOV-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Anderson, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2835-WO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEX: 756822
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 291 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US96-10895-6

[illegible]

```

1      RESULT          9
2      US-09-105-343A-8
3      Sequence 8, Application US/09105343A
4      Patent No. 6207642
5      GENERAL INFORMATION:
6      APPLICANT: WILEY, S.R.
7      TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
8      TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
9      NUMBER OF SEQUENCES: 12
10     CORRESPONDENCE ADDRESS:
11     ADDRESSEE: Abbott Laboratories
12     STREET: 100 Abbott Park Road
13     CITY: Abbott Park
14     STATE: IL
15     COUNTRY: USA
16     ZIP: 60064-6050
17     COMPUTER READABLE FORM:
18     MEDIUM TYPE: Diskette
19     COMPUTER: IBM Compatible
20     OPERATING SYSTEM: Windows
21     SOFTWARE: FASTSEQ for Windows Version 2.0b
22     CURRENT APPLICATION DATA:
23     APPLICATION NUMBER: US/09/105,343A
24     FILING DATE: 12-FEB-1998
25     CLASSIFICATION:
26     PRIOR APPLICATION DATA:
27     APPLICATION NUMBER: PCT/US98/02859
28     FILING DATE: 12-FEB-1998
29     ATTORNEY/AGENT INFORMATION:
30     NAME: BECKER, Cheryl L.
31     REGISTRATION NUMBER: 35,441
32     REFERENCE/DOCKET NUMBER: 6048.US.P2
33     TELECOMMUNICATION INFORMATION:
34     TELEPHONE: 847-935-1729
35     TELEFAX: 847-938-2623
36     TELEX:
37     INFORMATION FOR SEQ ID NO: 8:
38     SEQUENCE CHARACTERISTICS:
39     LENGTH: 183 amino acids
40     TYPE: amino acid
41     STRANDEDNESS: single
42     TOPOLOGY: linear
43     MOLECULE TYPE: NO. 6207642a
44     US-09-105-343A-8

```

Query Match	65.7%;	Score 654;	DB 4;	Length 183;
Best Local Similarity	68.7%;	Pred. NO. 4.9e-62;		
Matches 125;	Conservative 22;	Mismatches 29;	Indels 6;	Gaps 1

```
OY      15 EKOONISPLVBERGQOPAAAHITGRGSNLTSPNSNKNEALGRKINSNESSRSGHSFL 74
        III : | : |||III|   III : | : | : |||III| III|
Db      1 EKOLSTPPLPRGGRRQOKAAHIITGITRRSNALLPIISKDGTLOOKIESNESSRKHSHFL 60
OY      75 SNLHLRGSELVIHEKGFYIYSQTYPFRFOEB-----IKENTKNDKOMVOYIYKYTSPYD 128
        :: :|||III|:: |||III|III|
Db      61 NHVLFRNLGEIYEDGELTYIYSQTYPFRFOEADASKMWSKDVKRTKQLVGYIYKYTSPYD 120
OY      129 PILLMKSARNCSMSKSDATYGIXSYIOGIFELKLKNDDIPFSVTYNHEHILMDHDHSAFFGAF 168
        III|III|III|III|III|III|III|III|III|III|III|III|III|III|III|
Db      121 PIVLMKSARNCSMSKSDAYEGLYSYOGLEFELKLKNDRIFVSVYNHEHILMDDOESAFFGAF 180
OY      189 LV 190
        :: :|
Db      181 II 182
```

```

10 RESULT
11 US-08-996-139-11
12 ; Sequence 11, Application US/08996139
13 ; Patent No. 6017729
14 ; GENERAL INFORMATION:
15 ; APPLICANT : Anderson, Dirk M.
16 ; APPLICANT : Anderson, Galibert, Laurent
17 ; APPLICANT : Maraskovsky, Eugene
18 ; TITLE OF INVENTION: Receptor Activator of NF-kappaB
19 ; NUMBER OF SEQUENCES: 19
20 ; CORRESPONDENCE ADDRESS:
21 ; ADDRESSEE: Immunex Corporation, Law Department
22 ; STREET: 51 University Street
23 ; CITY: Seattle
24 ; STATE: WA
25 ; COUNTRY: USA
26 ; ZIP: 98101
27 ; COMPUTER READABLE FORM:
28 ; MEDIUM TYPE: Floppy disk
29 ; COMPUTER: Apple Power Macintosh
30 ; OPERATING SYSTEM: Apple Operating System 7.5.5
31 ; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
32 ; CURRENT APPLICATION DATA:
33 ; APPLICATION NUMBER: US/08/996,139
34 ; FILING DATE: 22 DECEMBER 1997
35 ; CLASSIFICATION:
36 ; PRIOR APPLICATION DATA:
37 ; APPLICATION NUMBER: USSN 60/064,671
38 ; FILING DATE: 14 OCTOBER 1997
39 ; PRIOR APPLICATION DATA:
40 ; APPLICATION NUMBER: USSN 08/813,509
41 ; FILING DATE: 07 MARCH 1997
42 ; PRIOR APPLICATION DATA:
43 ; APPLICATION NUMBER: USSN 08/772,330
44 ; FILING DATE: 23 DECEMBER 1996
45 ; ATTORNEY/AGENT INFORMATION:
46 ; NAME: Perkins, Patricia Anne
47 ; REGISTRATION NUMBER: 34,693
48 ; REFERENCE/DOCKET NUMBER: 2851-A
49 ; TELECOMMUNICATION INFORMATION:
50 ; TELEPHONE: (206)587-0430
51 ; TELEFAX: (206)233-0644
52 ; INFORMATION FOR SEQ ID NO: 11:
53 ; SEQUENCE CHARACTERISTICS:
54 ; LENGTH: 294 amino acids
55 ; TYPE: amino acid
56 ; TOPOLOGY: linear
57 ; MOLECULE TYPE: protein
58 ; US-08-996-139-11

```

Query Match	23.68;	Score 235.5;	DB 3;	Length 294;
Best Local Similarity	29.38;	Pred. No. 3,1e-17;		
Matches 65;	Conservative 37;	Mismatches 67;	Indels 53;	Gaps 7
Q1	6	SHEET-----	STVQEKQONISLVNDRGPVVA-----	33

DB 85 SEETLDPSCRMKQAFQAVQKELQHIIV-----GQRFSGAPAMMGSMWDVAORGPKE 138
QY 34 ---AHITGRGNSNTLSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVYIHER 89
DB 139 AOPFAHUT-----INAAISIPSGSHKVTL-----SSWYHDR-GWAKISNMTLSNCKLRVNOD 188
QY 90 GFIYIISQTYFRFOEIKENTKNDKQMVQIYKYT-SYDPILLMKSARNSCSKDAEYG 148
DB 189 GFYLLYANICFRHETSGSVPTDYQLMIVYVKTSLIKIPSHNLMKGSGTKMNSGSEFH 248
QY 149 LYSIYOGIFELKENDRIFVSVTNEHLIDMDHASFQAFV 190
DB 249 FYSINVGFFKLKAGEISLQVSNPSLLDPDODATYFGAFKV 290

RESULT 11
US-08-995-659-11
; Sequence 11, Application US/08995659
; Patent No. 6242213
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh.
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,659
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-995-659-11

Query Match 23.6%; Score 235.5; DB 4; Length 294;
Best Local Similarity 29.3%; Pred. No. 3.1e-17;
Matches 65; Conservative 37; Mismatches 67; Indels 53; Gaps 7;

QY 6 SEETI-----STVOEKQONISPLVREGQRYA----- 33
DB 85 SEETLDPSCRMKQAFQAVQKELQHIIV-----GQRFSGAPAMMGSMWDVAORGPKE 138
QY 34 ---AHITGRGNSNTLSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVYIHER 89
DB 139 AOPFAHUT-----INAAISIPSGSHKVTL-----SSWYHDR-GWAKISNMTLSNCKLRVNOD 188
QY 90 GFIYIISQTYFRFOEIKENTKNDKQMVQIYKYT-SYDPILLMKSARNSCSKDAEYG 148
DB 189 GFYLLYANICFRHETSGSVPTDYQLMIVYVKTSLIKIPSHNLMKGSGTKMNSGSEFH 248
QY 149 LYSIYOGIFELKENDRIFVSVTNEHLIDMDHASFQAFV 190
DB 249 FYSINVGFFKLKAGEISLQVSNPSLLDPDODATYFGAFKV 290

RESULT 12
US-08-842-842-7
; Sequence 7, Application US/08842842
; Patent No. 5843678
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavenland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91330-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,842
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-451
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-842-842-7

Query Match 23.6%; Score 235.5; DB 2; Length 316;
Best Local Similarity 29.3%; Pred. No. 3.5e-17;
Matches 65; Conservative 37; Mismatches 67; Indels 53; Gaps 7;

QY 6 SEETI-----STVOEKQONISPLVREGQRYA----- 33
DB 107 SEETLDPSCRMKQAFQAVQKELQHIIV-----GQRFSGAPAMMGSMWDVAORGPKE 160
QY 34 ---AHITGRGNSNTLSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVYIHER 89
DB 161 AOPFAHUT-----INAAISIPSGSHKVTL-----SSWYHDR-GWAKISNMTLSNCKLRVNOD 210
QY 90 GFIYIISQTYFRFOEIKENTKNDKQMVQIYKYT-SYDPILLMKSARNSCSKDAEYG 148
DB 211 GFYLLYANICFRHETSGSVPTDYQLMIVYVKTSLIKIPSHNLMKGSGTKMNSGSEFH 270
QY 149 LYSIYOGIFELKENDRIFVSVTNEHLIDMDHASFQAFV 190
DB 271 FYSINVGFFKLKAGEISLQVSNPSLLDPDODATYFGAFKV 312

RESULT 13

US-08-989-362-2

Sequence 2, Application US/08989362

Patent No. 6242586

GENERAL INFORMATION:

APPLICANT: Gorman, Daniel M.

APPLICANT: Mattson, Jeanine D.

TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related

TITLE OF INVENTION: Reagents

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/989,362

FILING DATE: 12-DEC-1997

CLASSIFICATION: 56

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/032,846

FILING DATE: 13-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0686

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650)852-9196

TELEFAX: (650)496-1204

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 316 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-989-362-2

Query Match 23.6%; Score 235.5; DB 4; Length 316;

Best Local Similarity 29.3%; Pred. No. 3.5e-17;

Matches 65; Conservative 37; Mismatches 67; Indels 53; Gaps 7;

QY	6	SEPTI-----STVOEKQONISPLVERGPOVA-----	33
	11:1	11:1	11:1

DB	107	SEDTLPSCRRMKQAFQAGVKELOHIV-----GPQRFSGAPAMEGSWLDVAQRKPE	160
	11:1	11:1	11:1

QY	34	---AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNGELVIEHK	89
	11:1	11:1	11:1

DB	161	AQPAHLH-----INAAISIPGSHKVTL-----SSWYHDR-GWAKISNMTLSNGKLRYMOD	210
	11:1	11:1	11:1

QY	90	GFYIYSOTYRFOEIKENTKNDKQOVYIKYKT-SYDPDILMKSAKNSCWSKDAEYG	148
	11:1	11:1	11:1

DB	211	GFYLYLVANICFRHHTSGSVPTDYLQLMVYVVKTSIKIPSSHNLKMGSGTKNWSGNSFEH	270
	11:1	11:1	11:1

QY	149	LXSTYOGCIFELKENDRIEVSVTNEHLIDMDHEASFGAFIV	190
	11:1	11:1	11:1

DB	271	FYSINVGGFELRAGEEISIVSNPSLDDPDQDATYFGAFKV	312
	11:1	11:1	11:1

RESULT 14

US-08-996-139-13

Sequence 13, Application US/08996139

Patent No. 6017729

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

APPLICANT: Galibert, Laurent

APPLICANT: Maraskovsky, Eugene

TITLE OF INVENTION: Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Apple Power Macintosh

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/996,139

FILING DATE: 22 DECEMBER 1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 60/064,671

FILING DATE: 14 OCTOBER 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2851-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 317 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-996-139-13

Query Match 23.3%; Score 232.5; DB 3; Length 317;

Best Local Similarity 32.9%; Pred. No. 7.2e-17;

Matches 52; Conservative 33; Mismatches 62; Indels 11; Gaps 4;

QY	34	AHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNGELVIEHKFY	93
	11:1	11:1	11:1

DB	166	AHLT-----INATDIPSSHKVSL-----SSWYHDR-GWAKISNMTFSNGKLIVNODGFY	215
	11:1	11:1	11:1

QY	94	IYSOTYRFOEIKENTKNDKQOVYIKYKT-SYDPDILMKSAKNSCWSKDAEGLYSI	152
	11:1	11:1	11:1

DB	216	LYANICFRHHTSGDLATIEYQLMVYVVKTSIKIPSSHNLKMGSGTKYWSGNSERHFSI	275
	11:1	11:1	11:1

QY	153	YOGCIFELKENDRIEVSVTNEHLIDMDHEASFGAFIV	190
	11:1	11:1	11:1

DB	276	NVGGFELRAGEEISIVSNPSLDDPDQDATYFGAFKV	313
	11:1	11:1	11:1

RESULT 15

US-08-995-659-13

Sequence 13, Application US/08995659

Patent No. 6242213

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

APPLICANT: Galibert, Laurent

APPLICANT: Maraskovsky, Eugene

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Immunex Corporation, Law Department
;; STREET: 51 University Street
;; CITY: Seattle
;; STATE: WA
;; COUNTRY: USA
;; ZIP: 98101
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Power Macintosh
;; OPERATING SYSTEM: Apple Operating System 7.5.5
;; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/995,659
;; FILING DATE: 22 DECEMBER 1997
;;
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 60/064,671
;; FILING DATE: 14 OCTOBER 1997
;;
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 08/813,509
;; FILING DATE: 07 MARCH 1997
;;
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 08/772,330
;; FILING DATE: 23 DECEMBER 1996
;;
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,693
;; REFERENCE/DOCKET NUMBER: 2852-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)233-0644
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 317 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
;; US-08-995-659-13

Query Match 23.3%; Score 232.5; DB 4; Length 317;
Best Local Similarity 32.9%; Pred. No. 7.2e-17;
Matches 52; Conservative 33; Mismatches 62; Indels 11; Gaps 4;
QY 34 AHITGRGRSNTLSSPNSKNEKALGRKINWESSRSGHSLNLHLRNGELVIHEKGFY 93
DB 166 AHIT-----INATDIPSGSHKSL---SSWYHDR-GWAKISNMTPSNGKLIYNODGFY 215
QY 94 IYEQTYFRFOEIEIKENWKNDKQWQYIKYT-SYDPILMKSAKNSCWKDAEYGLYSI 152
DB 216 LVNINICFRHHTETGDLATELQLMVYVTKSIKIPSSHLMKGGSTKYWNGNSEPHFYI 275
QY 153 YGGIFELKENDRIEVSVTNEHLIDMDHEASFGAFYV 190
DB 276 NVGGFFKLRSGEISIEVSNPILDPDQATYFGAFKV 313

Search completed: October 1, 2001, 11:43:33
Job time: 109 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 1, 2001, 11:40:13 ; Search time 20.84 Seconds

(without alignments)
555.623 Million cell updates/sec

Title: US-09-479-252-1_COPY_91_281

Perfect score: 996

Sequence: 1 MLPTSEETISTVQEKQONI.....NEHLIDMDHEASFGAFIVG 191

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601:*

1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT:*

2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT:*

3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT:*

4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT:*

5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT:*

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9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT:*

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12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT:*

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14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT:*

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16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT:*

17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT:*

18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT:*

19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT:*

20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT:*

21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT:*

22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	996	100.0	279	19	AAW76332
2	996	100.0	279	20	AAW95032
3	996	100.0	281	18	AAW27134
4	996	100.0	281	18	AAW19787
5	996	100.0	281	18	AAW19777
6	996	100.0	281	19	AAW76829
7	996	100.0	281	19	AAW56760
8	996	100.0	281	19	AAW44354
9	996	100.0	281	20	AAW27012
10	996	100.0	281	20	AAW01517
11	996	100.0	281	21	AAW28691

12	996	100.0	281	21	AAW24038	Human PRO1096 prot
13	996	100.0	281	21	AAW08545	Amino acid sequenc
14	996	100.0	281	21	AAW81956	Human Apo-2 ligand
15	996	100.0	281	22	AAW8350	Human TL2 polypept
16	996	100.0	281	22	AAW67243	Human Apo2 ligand.
17	996	100.0	281	22	AAW50977	Human PRO1096 prot
18	989	99.3	281	20	AAW01516	Protein associated
19	988	99.2	281	20	AAW27016	Human Apo-2 ligand
20	988	99.2	281	20	AAW27017	Human Apo-2 ligand
21	988	99.2	281	20	AAW27018	Human Apo-2 ligand
22	974	97.8	281	21	AAW28692	Human Apo-2 ligand
23	972	97.6	281	20	AAW27019	Human Apo-2 ligand
24	953.5	95.7	220	21	AAW86630	Cell factor deriva
25	893.5	89.7	423	21	AAW28693	Fc-huAcp-1 (114-28
26	878	88.2	166	21	AAW08274	Amino acid sequenc
27	850	85.3	161	22	AAW71985	C-terminal region
28	727	73.0	139	20	AAW01518	Polypeptide of the
29	693	69.6	291	18	AAW19788	Mouse apoptosis in
30	693	69.6	291	19	AAW56762	Murine TRAIL polyp
31	693	69.6	291	19	AAW4353	Murine AGP-1. Mus
32	686	68.9	448	21	AAW28694	Fc-muAcp-1 (99-291
33	639.5	64.2	426	21	AAW28695	Amino acid sequenc
34	633	63.6	172	21	AAW08275	Mouse ODF-bind
35	235.5	23.6	244	19	AAW83019	NF-KB receptor act
36	235.5	23.6	294	19	AAW69956	NF-KB receptor act
37	235.5	23.6	294	19	AAW68292	Human osteoprotege
38	235.5	23.6	316	19	AAW83194	Osteoclastogenesis
39	235.5	23.6	316	19	AAW83017	Murine TRANCE. Mu
40	235.5	23.6	316	19	AAW59654	Amino acid sequenc
41	235.5	23.6	316	21	AAW17874	Mouse OBM protein
42	235.5	23.6	316	21	AAW91024	Amino acid sequenc
43	235.5	23.6	316	21	AAW84418	Amino acid sequenc
44	235.5	23.6	316	21	AAW84419	Amino acid sequenc
45	232.5	23.3	152	22	AAW67248	Human RANKL. Homo

ALIGNMENTS

RESULT	1
AAW76332	standard; Protein: 279 AA.
ID	AAW76332
XX	AAW76332;
AC	AAW76332;
XX	
DT	11-JAN-1999 (first entry)
XX	
DE	Human TL2 (TRAIL), ligand for TR5.
XX	
KW	TL2; TRAIL; tumor necrosis related receptor; TR5; inflammation;
KW	arthritis; septicaemia; transplant rejection; autoimmune disease;
KW	inflammatory bowel disease; graft versus host disease; infection;
KW	stroke; ischaemia; acute respiratory disease syndrome; psoriasis;
KW	retinosis; brain injury; AIDS; bone disease; cancer;
KW	atherosclerosis; Alzheimer's disease; human; therapy; diagnosis;
KW	ligand.
XX	
OS	Homo sapiens.
XX	
PN	EP867509-A2.
XX	
PD	30-SEP-1998.
XX	
PF	04-FEB-1998; 98EP-0300827.
XX	
PR	28-JUL-1997; 97US-0901469.
PR	05-FEB-1997; 97US-0795910.
XX	
PA	(SMIK) SMITHKLINE BEECHAM CORP.
XX	
PI	Lyn SDP, Tan KB, Truneh A, Young PR;
XX	
DR	WPI; 1998-497862/43.

PN M09733899-A1.
 XX 18-SEP-1997.
 PD
 XX
 PF 14-MAR-1996; 96WO-US03773.
 XX
 PR 14-MAR-1996; 96WO-US03773.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM;
 DR WPI: 1997-470807/43.
 DR N-PSDB; AAT85210.
 XX
 PT New isolated apoptosis inducing molecule-I - used to develop
 PT products for the diagnosis and therapy of e.g. autoimmune diseases,
 PT tumours, graft versus host disease or inflammation.
 PS
 PS Claim 2; Fig 1; 82pp; English.
 XX
 CC The present sequence represents a human Apoptosis inducing molecule-I
 CC (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand
 CC superfamily. The products can be used in the diagnosis and treatment of
 CC disorders related to under-expression, over-expression or altered
 CC expression of AIM-I. AIM-I or agonists can be used for treating
 CC autoimmune disorders including systemic lupus erythematosus,
 CC immunoproliferative disease lymphadenopathy (ILD),
 CC angioimmunoproliferative lymphadenopathy (AID), rheumatoid arthritis,
 CC diabetes, and multiple sclerosis, graft versus host disease, to inhibit
 CC neoplasia such as tumour cell growth, to treat restenosis, to regulate
 CC haematopoiesis in endothelial cell development, to stimulate peripheral
 CC tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be
 CC used for treating cachexia, cerebral malaria, rheumatoid arthritis
 CC or osteoporosis, for preventing graft-host rejection, and as
 CC anti-inflammatory agents, for treating endotoxic shock or to prevent
 CC activation of HIV.
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 996; DB 18; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.4e-94;
 Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;
 XX thrombotic microangioplasty; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..18
 FT /label= Cytoplasmic_domain
 FT 19..38
 FT /label= Transmembrane_domain
 FT 39..281
 FT /label= Extracellular_domain
 FT /note= "contains a receptor-binding region"
 FT 109..111
 FT /note= "potential N-glycosylation site"
 FT 89..90
 FT /note= "potential KEX2 protease processing site"
 FT 149..150
 FT /note= "potential KEX2 protease processing site"
 FT
 FT Cleavage-site
 FT
 XX M09701633-A1.
 XX
 XX 16-JAN-1997.
 PD
 XX
 PF 25-JUN-1996; 96WO-US10895.
 XX
 PR 01-NOV-1995; 95US-0548368.
 PR 29-JUN-1995; 95US-0496632.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Goodwin RG, Wiley SR;
 XX WPI: 1997-118715/11.
 DR N-PSDB; AAT72847.
 DR
 XX
 PT TRAIL, a novel cytokine, induces apoptosis in cancer and
 PT virus-infected cells - useful for treating thrombotic
 PT microangiopathy, cancer and viral infection and for use in assays
 XX
 XX Claim 10; Page 43-44; 62pp; English.
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 996; DB 18; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.4e-94;
 Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 271 easfifaflvg 281

RESULT 5

AAW19777

ID AAW19777 standard; Protein; 281 AA.

AC AAW19777;

DT 22-SEP-1997 (first entry)

DE Novel cytokine Apo-2 ligand.

KW Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Peptide 1..281

FT Protein /note="Claim 4"

FT Protein /note="Claim 3"

FT Protein /note="Claim 2"

FT Protein /note="Claim 1"

FT Region /label="Cytoplasmic-region

FT Region 15..40

FT Region /label="Transmembrane-region

FT Region 41..281

FT Modified-site /label="Extracellular-region

FT /label="glycosylation

FT /note="putative N-linked glycosylation site"

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Query Match 100.0%; Score 996; DB 18; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.4e-94; Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MILRTSEETSTVOEQOONISPLVREGRPOVAHAHTGTGRCGRNTLSSPSKNEKLGK 60

Db 91 mlrtseetstvqeqnslplvregprvaahltgtrgrntlsspskneka1gk 150

QY 61 INSMESRSCHSFLSNLNLNGELVHEKGFYIYSQTFRFOEIKENTKNDKQVOYI 120

Db 151 insmesrsghsflsnlhlngelvlhekgfyllsqtyfrfgeelkentkndkqmvqy 210

QY 121 YKTTSTYDPDPLLMKSARNCSWSDAEGYLSITQGIPELKEKDRIFVSYTNEHLIDMH 180

Db 211 yktsypdpillmksarnscswskaeaylysggylfelkendrlfsvtnehlidmh 270

QY 181 EASFPGALVIG 191

Db 271 easfifaflvg 281

RESULT 6

AAW76829

ID AAW76829 standard; Protein; 281 AA.

AC AAW76829;

DT 25-JAN-1999 (first entry)

DE Human TL2 protein.

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Query Match 100.0%; Score 996; DB 18; Length 281;

Disclosure: Page 32-33; 34pp: English.

PT DNA encoding tumour necrosis factor receptor TR6 - and corresponding polypeptide, antibody, agonist, antagonist, etc

PS

XX

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XX

Query Match 100.0%; Score 996; DB 18; Length 281;

This sequence represents the human tumour necrosis factor (TNF)-related receptor, TL2 (also known as tumour necrosis factor-related apoptosis-inducing ligand, TRAIL). This protein is used in a method

resulting in the isolation of the novel human TNF related receptor, TR6. TR6 polypeptides and polynucleotides can be used in the treatment of

chronic and acute inflammation, arthritis, septicemia, autoimmune

diseases (e.g. inflammatory bowel disease, psoriasis), transplant

rejection, graft vs. host disease, infection, stroke, ischaemia, acute

respiratory disease syndrome, restenosis, brain injury, (acquired

autoimmune disease syndrome) AIDS, bone diseases, cancer (e.g.

lympho-proliferative disorders), atherosclerosis and Alzheimers disease.

XX

XX

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XX

XX

SQ Sequence 281 AA;
 Query Match 100.0%; Score 996; DB 19; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.4e-94;
 Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MILRTSETISTVOEKQONISPLVREGRQVAAHITGRKSRNTLSSPNKNEKALGRK 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 91 mlrtsetistlvqekqgnslpvrerqpgvaahltqtrgrntlsspsnknekalgrk 150
 QY 61 INSWESSRSGHSFSLNHLRNGELVIEHKGFYIYSQTYFRFOEIKENTKNDKQWYI 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 151 inswessrsghsfslnhlringelvihekgyfyyisqtyfrfgeekentkndkqmwyl 210
 QY 121 YKRTSYDPDPLILMKSAKNSCKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDH 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 211 ykrtsydpdplllmksarncswkdaeyglysiyggifelkendriffsvenehlidmdh 270
 QY 181 EASFECAFLVG 191
 ||||||||||||
 DB 271 easfifgaflvg 281
 RESULT 7
 AAM56760
 ID AAM56760 standard; Protein: 281 AA.
 AC AAM56760;
 XX
 DT 05-AUG-1998 (first entry)
 XX
 DE Human TRAIL polypeptide.
 KW Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;
 XX cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..18
 FT /note= "N-terminal cytoplasmic domain"
 FT Region 19..38
 FT /note= "transmembrane region"
 FT Domain 39..281
 FT /note= "extracellular domain"
 XX
 PN US5763223-A.
 XX
 PD 09-JUN-1998.
 XX
 PF 25-JUN-1996; 96US-0670354.
 XX
 PR 25-JUN-1996; 96US-0670354.
 PR 29-JUN-1995; 95US-0496632.
 PR 01-NOV-1995; 95US-0548368.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Goodwin RG, Willey SR;
 XX
 DR WPI: 1998-347332/30.
 DR N-PSDB: AAV29518.
 XX
 PT DNA encoding cytokine TNF-related apoptosis ligand polypeptides -
 PT useful for producing recombinant polypeptides for research and
 PT therapy of leukaemia, lymphoma, melanoma and viral infections
 XX
 PS Claim 1; Columns 33-36; 28pp; English.
 XX
 CC This represents a human tumour necrosis factor related apoptosis ligand
 CC (TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce
 CC apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful

CC for producing the recombinant TRAIL polypeptides, which may be useful in
 CC studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells
 CC (e.g. to isolate antigens for vaccine development). The polypeptides can
 CC be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal
 CC treatment of blood or bone-marrow), or to treat viral infections.
 CC
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 996; DB 19; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.4e-94;
 Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MILRTSETISTVOEKQONISPLVREGRQVAAHITGRKSRNTLSSPNKNEKALGRK 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 91 mlrtsetistlvqekqgnslpvrerqpgvaahltqtrgrntlsspsnknekalgrk 150
 QY 61 INSWESSRSGHSFSLNHLRNGELVIEHKGFYIYSQTYFRFOEIKENTKNDKQWYI 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 151 inswessrsghsfslnhlringelvihekgyfyyisqtyfrfgeekentkndkqmwyl 210
 QY 121 YKRTSYDPDPLILMKSAKNSCKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDH 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 211 ykrtsydpdplllmksarncswkdaeyglysiyggifelkendriffsvenehlidmdh 270
 QY 181 EASFECAFLVG 191
 ||||||||||||
 DB 271 easfifgaflvg 281
 RESULT 8
 AAM44354
 ID AAM44354 standard; Protein: 281 AA.
 AC AAM44354;
 XX
 DT 28-MAY-1998 (first entry)
 XX
 DE Human AGP-1.
 KW Human; AGP-1; tumour necrosis factor-related protein; TNF;
 XX inflammation; bone resorption; haematopoietic disease.
 OS Homo sapiens.
 XX
 PN WO9746686-A2.
 XX
 PD 11-DEC-1997.
 XX
 PF 06-JUN-1997; 97MO-US09895.
 XX
 PR 07-JUN-1996; 96US-0660562.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Danilenko DM, Johnson MJ, Simonet WS;
 XX
 DR WPI: 1998-042194/04.
 DR N-PSDB: AAV15295.
 XX
 PT Nucleic acid encoding AGP-1, a tumour necrosis factor-related
 PT protein - useful for creating inflammation, bone resorption and
 PT haematopoietic diseases
 XX
 PS Claim 7; Page 36-37; 54pp; English.
 XX
 CC The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis
 CC factor (TNF)-related protein, involved in inflammation, myelopoiesis
 CC and bone resorption. It has the same nucleic acid and amino acid (aa)
 CC sequences as the TNF-related apoptosis-induced ligand (TRAIL) described
 CC in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay
 CC reagents for detecting AGP-1 expression. Nucleic acid complementary to
 CC AGP-1 is used to regulate AGP-1 expression and antagonistic compounds

CC of degenerative, autoimmune and inflammatory diseases. The polypeptides
CC can be used in treatment of neurodegenerative disease, lupus
CC erythematous, rheumatoid arthritis, and SEP. The polypeptides are
CC apoptotic in central nervous system cells, antigenic and specifically
CC recognise the surface receptor of the TRAIL protein. The polypeptide is
CC a marker of disease and a therapeutic target, e.g. its apoptotic activity
CC can be blocked with an anti-TRAIL antibody or a TRAIL equivalent that
CC binds to specific receptors, inhibiting formation of natural complex.

XX Sequence 281 AA:

Query Match 100.0%; Score 996; DB 20; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.4e-94;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIIKTSEETISTVOEKQONISPLVREKGPQVAHAHTGTRGRSNTLSSPSNKEKALGRK 60
DB 91 MIITSEETISTVGEKQNSPLVREKGPQVAHAHTGTRGRSNTLSSPSNKEKALGRK 150
QY 61 INWESSRSGHSFLSNHLRNGELVHEKGFYIYSQTYRFOEIKENTKNDKQWYI 120
DB 151 INWESSRSGHSFLSNHLRNGELVHEKGFYIYSQTYRFOEIKENTKNDKQWYI 210
QY 121 YKTSYDPDILLMKSAKNSCKDAEYGLYSIYGIFELKENDRIFVSVTNEHLIDMDH 180
DB 211 YKTSYDPDILLMKSAKNSCKDAEYGLYSIYGIFELKENDRIFVSVTNEHLIDMDH 270
QY 181 EASFFGAFIVG 191
DB 271 EASFFGAFIVG 281

RESULT 11

AAB28691 standard; Protein; 281 AA.

XX AAB28691;

DT 14-FEB-2001 (first entry)

XX Human AGP-1.

XX Human; AGP-1; type II transmembrane protein; cytosolic; antiviral;
KM antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;
KM human immunodeficiency virus; apoptosis; proliferative disorder;
KM cancer; hepatitis; acquired immunodeficiency syndrome; AIDS;
KM autoimmune disorder; transplant rejection; cardiovascular disease;
arteriosclerosis.

XX Homo sapiens.

XX WO200063253-A1.

PD 26-OCT-2000.

PF 24-MAR-2000; 2000MO-US08004.

PR 16-APR-1999; 99US-0293245.

PA (AMGE-) AMGEN INC.

PI Hsu H, Meng S;

DR WPI; 2000-665240/64.

DR N-PSDB; AAC67831.

PT Fusion protein of AGP-1 protein and an FC region, used to treat
PT proliferative disorders, immune disorders, and virally-induced
PT disorders

XX Claim 3; Fig 2; 93pp; English.

CC The present sequence is human AGP-1, a type II transmembrane protein.
CC Fusion proteins comprising an FC immunoglobulin region fused to the
CC N-terminal portion of the AGP-1 protein have been produced. The fusion
CC proteins can be used to induce apoptosis in a tissue, and to treat
CC proliferative disorders, immune disorders, or virally-induced disorders.
CC The proliferative disorders include cancers, such as breast, prostate,
CC lung or colon cancer. The viral infections include hepatitis, and
CC acquired immunodeficiency syndrome (AIDS), and the immune disorders may
CC be autoimmune disorders or transplant rejection. Cardiovascular
CC diseases such as arteriosclerosis may also be treated. The
CC AGP-1 containing fusion proteins have increased biological activity
CC compared to the soluble AGP-1 proteins used in prior art therapies.

XX Sequence 281 AA:

Query Match 100.0%; Score 996; DB 21; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.4e-94;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIIKTSEETISTVOEKQONISPLVREKGPQVAHAHTGTRGRSNTLSSPSNKEKALGRK 60
DB 91 MIITSEETISTVGEKQNSPLVREKGPQVAHAHTGTRGRSNTLSSPSNKEKALGRK 150
QY 61 INWESSRSGHSFLSNHLRNGELVHEKGFYIYSQTYRFOEIKENTKNDKQWYI 120
DB 151 INWESSRSGHSFLSNHLRNGELVHEKGFYIYSQTYRFOEIKENTKNDKQWYI 210
QY 121 YKTSYDPDILLMKSAKNSCKDAEYGLYSIYGIFELKENDRIFVSVTNEHLIDMDH 180
DB 211 YKTSYDPDILLMKSAKNSCKDAEYGLYSIYGIFELKENDRIFVSVTNEHLIDMDH 270
QY 181 EASFFGAFIVG 191
DB 271 EASFFGAFIVG 281

RESULT 12

AAB24038 standard; Protein; 281 AA.

XX AAB24038;

DT 25-JAN-2001 (first entry)

XX Human PRO1096 protein sequence SEQ ID NO:51.

XX Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
KM identification; tumourigenesis; anticancer; detection.

XX Homo sapiens.

XX WO200053750-A1.

PD 14-SEP-2000.

PF 02-DEC-1999; 99WO-US28551.

PR 08-MAR-1999; 99WO-US05028.

PR 01-SEP-1999; 99WO-US20111.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99WO-US28313.

PR 01-DEC-1999; 99WO-US28634.

PA (GETH) GENENTECH INC.

DR WPI; 2000-594320/56.

DR N-PSDB; AAC58120.

PT Antibodies specific for PRO polypeptides, used to diagnose and inhibit
PT the growth of tumors in mammals, and to identify inhibitors of PRO

DR WPI: 2000-282690/24.
DR N-PSDB: AAA07425.
XX
PT New isolated monoclonal antibodies having antigen specificity for Apo-2
PT ligand, e.g. 266, 2E11 or 5C2, useful for detecting the expression of
PT Apo-2 ligand serum, and for treating diseases associated with increased
PT apoptosis -
XX
PS Claim 9: Fig 1a: 46pp: English.
XX
CC This sequence is the human Apo-2 ligand protein, which is recognised
CC by monoclonal antibodies produced by the hybridoma cell lines of the
CC invention. The hybridoma cell lines are deposited under the American Type
CC Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258
CC and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic
CC assays for Apo-2 ligand, e.g. detecting its expression in specific cells,
CC tissues, or serum. The antibodies may also be employed as therapeutics.
CC For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand
CC activity, like Apo-2 ligand-induced apoptosis, may be employed to treat
CC pathological conditions or diseases associated with increased
CC apoptosis. They are also useful for the affinity purification of Apo-2
CC ligand from recombinant cell culture or natural sources. The Apo-2
CC ligand itself may be used to treat diseases e.g. cancer, by inducing
CC apoptosis in cells.
CC
XX
SQ Sequence 281 AA:

Query Match 100.0%; Score 96; DB 21; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.4e-94;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MILRTSETISTVOEKQONISPLVREGRPOVAAHITGTRGRSNTLSPNSKNEKALGRK 60
DB 91 mlrtseeltstvyqekgnspivrerqpvaahtlgtgrsntlsspsnkeakalgrk 150
QY 61 INSWESSRSGHSFLSNLHNLNGELVIEHEKGFYIYSOTYRFFOEIKENTKNDKQMYI 120
DB 151 inswessrsghsfslsnhlrnlngelvhnekgyfyytsqlyfrfgeekentkndqmyyi 210
QY 121 YKTSYDPDPIILKMSARNSCSKDAEYGLYSYOGGIFELKENDRIFVSVTNEHLIDMDH 180
DB 211 yktsypdpdillmksarnscwskdaeyglysyggifelkendrifsvtnehlidmdh 270
QY 181 EASFGAFIVG 191
DB 271 easfgafivg 281

RESULT 15
AAB48350
ID AAB48350 standard: Protein; 281 AA.
XX
AC AAB48350;
XX
DT 20-APR-2001 (first entry)
XX
DE Human TL2 polypeptide.
XX
XX Tumour necrosis factor; TNF; TNF related receptor; TR6; human; TL2;
KW antiinflammatory; immunosuppressive; cerebroprotective; vasotrophic;
KW antiasthmatic; anti-HIV; osteopathic; cytostatic; antithrombotic;
KW nootropic; neuroprotective; antiarthritic; antineumatic; antischismic;
KW gene therapy; vaccine; TNF-alpha; bone disease; cancer; TRAIL.
OS Homo sapiens.
XX
PN WO200077191-A1.
XX
PD 21-DEC-2000.
XX
PF 12-JUN-2000; 2000WO-US16134.
XX

PR 15-JUN-1999; 9905-0333593.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX
PT Deen KC, Young PR, Marshall LA, Roshak AK, Tan KB, Truneh A;
XX
DR WPI: 2001-112223/12.
DR N-PSDB: AAC84745.
XX
XX New tumor necrosis factor related receptor TR6 polynucleotides and
PT polypeptides useful for e.g. for treating chronic and acute
PT inflammation, arthritis, septicemia, autoimmune diseases, infection,
PT cancer, bone diseases -
XX
PS Disclosure: Page 26; 47pp: English.
XX
CC The invention relates to a human tumour necrosis factor (TNF) related
CC receptor, TR6. TR6 can be expressed by standard recombinant methodology.
CC The TR6 polypeptides are useful for treating chronic and acute
CC inflammation, rheumatoid arthritis, septicemia, autoimmune diseases
CC (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft
CC vs. host disease, infection, stroke, ischaemia, acute respiratory disease
CC syndrome, asthma, restenosis, brain injury, AIDS, bone diseases, cancer,
CC atherosclerosis, and Alzheimer's disease. These may also be used to
CC inhibit production of TNF-alpha and eicosanoids, as research reagents and
CC materials for discovering treatments and diagnostics to animal and human
CC diseases. The polypeptides may further be used as immunogens to produce
CC antibodies immunospecific for the TR6 polypeptides. The polynucleotides
CC may also be used as hybridization probes for cDNA and genomic DNA, for
CC isolating full-length cDNAs and genomic clones encoding TR6 and of other
CC genes having high sequence similarity to TR6 gene, and for chromosome
CC identification. The present sequence represents a human TL2 polypeptide.
CC TL2 is also known as TRAIL (TNF-related apoptosis-inducing ligand) and is
CC a ligand for the TL2 polypeptide.
CC
XX
SQ Sequence 281 AA:

Query Match 100.0%; Score 96; DB 22; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.4e-94;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MILRTSETISTVOEKQONISPLVREGRPOVAAHITGTRGRSNTLSPNSKNEKALGRK 60
DB 91 mlrtseeltstvyqekgnspivrerqpvaahtlgtgrsntlsspsnkeakalgrk 150
QY 61 INSWESSRSGHSFLSNLHNLNGELVIEHEKGFYIYSOTYRFFOEIKENTKNDKQMYI 120
DB 151 inswessrsghsfslsnhlrnlngelvhnekgyfyytsqlyfrfgeekentkndqmyyi 210
QY 121 YKTSYDPDPIILKMSARNSCSKDAEYGLYSYOGGIFELKENDRIFVSVTNEHLIDMDH 180
DB 211 yktsypdpdillmksarnscwskdaeyglysyggifelkendrifsvtnehlidmdh 270
QY 181 EASFGAFIVG 191
DB 271 easfgafivg 281

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Job time: 181 sec

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ID      09R1Y0      PRELIMINARY;      PRT;      313 AA.
AC      09R1Y0.
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE      OSTEOCLAST DIFFERENTIATION FACTOR.
OS      Mus musculus (Mouse).
OC      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX      NCBI_TaxId=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129;
RX      MEDLINE=99214075; PubMed=10196481;
RA      Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
RA      Ueda M., Higashio K.;
RT      "Cloning and characterization of the gene encoding mouse osteoclast
RT      differentiation factor.";
RL      Gene 230:121-127(1999).
DR      EMBL; AB022039; BAA36970.1; -.
DR      EMBL; AB022036; BAA36970.1; JOINED.
DR      EMBL; AB022037; BAA36970.1; JOINED.
DR      EMBL; AB022038; BAA36970.1; JOINED.
DR      InterPro; IPR000478; -.
DR      Pfam; PF00229; TNF; 1.
DR      PROSITE; PS00049; TNF 2; 1.
DR      SMART; SM00207; TNF; 1.
SQ      SEQUENCE 313 AA; 34719 MW; 37D530B8BFC2842E CRC64;

```

[illegible]

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50 SEQUENCE 287 AA; 32234 MW; 8B2CE8E4C7B534CC CRC64;

Query Match 23.6%; Score 235.5; DB 11; Length 287;
Best Local Similarity 29.3%; Pred. No. 2.8e-13;
Matches 65; Conservative 37; Mismatches 67; Indels 53; Gaps 7;

QY 6 SEET-----STVOEKOONISPLVREBPORVA-----33
   ||:|: ||:|:|
Db 78 SEDTLPDSCRNRKQAFQAGVORELDHIV-----GPORSGAPAMEGSMLDVAORQPE 131

QY 34 ----AHITGGRSNTLSSPSNKNKAKLGRKINSWESSRSGHPLSNLHNGELVIEHK 89
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 132 AQPFHNL-----IQAASIPSGSHVLT-----SSMYHDR-GWAKLSNMTLSNGKRLVQMD 181

QY 90 GFYIYISQTYRFRFOELIKENTKNDKQMOYIYKTY-STPDPILMKSRNNSCWGSDAEYG 148
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 182 GFYIYLAIACIRHNHETSGSVPTDYLTQLMVYVVKSIKIPSSNLMKGGSTKNWGSNSEFH 241

QY 149 LYSIVOGIFELKENDRIFFVSTNTHLMDMHESFGAFV 190
   ||| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 242 FYSLINVGSEFKLRAGEELISIOVSNPSLDDPODATTFFAFKY 283

```

RESULT 4		PRELIMINARY:		PRT: 199 AA.	
09JUK8	ID	09JUK8			
AC	09JUK8				
DT	01-OCT-2000	(TREMBLrel. 15, Created)			
DT	01-OCT-2000	(TREMBLrel. 15, last sequence update)			
DT	01-MAR-2001	(TREMBLrel. 16, last annotation update)			
DE	RECEPTOR ACTIVATOR OF NF-KB LIGAND 3.				
GN	RANKL 3.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Ikeda T., Takahashi H., Hirokawa K.;				
RT	"Somatostatin, a new marker of osteoblast, regulates the expression of				
RT	RANKL isoforms."				
RL	Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL; AB032772; BAA97258.1; -.				
DR	InterPro: IPR000478; -.				
DR	InterPro: IPR003263; -.				
DR	Pfam: PF00229; TNF: 1.				
DR	ProDom: PD006800; -;1				
DR	PROSITE: PSS00049; TNF_2: 1.				
SO	SEQUENCE 199 AA; 2150 MW; 401C13EB58CE166 CRC64;				

[illegible]

Query Match	Best Local Similarity	Matches	64; Conservative	35; Mismatches	68; Indels	31; Gaps
13 VOEKQONISPLVREKGPOR	23.3%;	Score 232.5;	DB 11;	Length 318;		
128 VORELOHIV	32.3%;	Pred. No. 5.9e-13;				
54 EKALGRKINSWESSRSGSFLSNLHLRNGELVHKGFFYIYSQTYRPFQEEIKENTKD	113					
182 KYSL	-----SWWHR-GWAKISNMTLSNCKLRVNDGFFYLALNLCFRHHETSGSVADY	236				
114 KOMVOYIKYT	SYDPILLMKASRNSCKDAEYGLYSIYGGIPELKEKENDRIFVSTN	172				
237 LQLMVYVVKTSIKIPSSHLMKSGSTKMWGSEFFHFYSINVGFFKPLRAGEEISYOVSN	296					
173 EHLIDMHEASPEGAFLV	190					
297 PSLDPPDDADYEGAFKV	314					
RESULT 6						
09MYL6	PRELIMINARY;	PRT:	280 AA.			
AC 01-MAR-2001 (TREMBlrel. 16, Created)						
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)						
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)						
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)						
DE RECEPTOR ACTIVATOR OF NF-KB LIGAND.						
OS Rattus norvegicus (Rat).						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.						
NCBI_TaxID=10116;						
SEQUENCE FROM N.A.						
Pubmed=11092398;						
Xu J.K., Tan J., Huang L., Gao X.H., Laird R., Liu D., Wyszocki S.,						
Zheng M.H.;						
"Cloning, sequence and functional characterization of the rat						
homologue of receptor activator of NF-kB ligand."						
J. Bone Miner. Res. 15:2178-2186(2000).						
EMBL; AF187319; AAG17031.1.						
SEQUENCE 318 AA; 35370 MW; 4B87AD706AD098 CRC64;						

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RN      [3]
RP      SEQUENCE FROM N.A. STRAIN-RHESUS MONKEY;
RC      SPECIES=M.mulatta;
RA      Kiril Y., Inoue T., Yoshino K.;
RT      "Rhesus monkey Fas ligand mRNA, complete cds.";
RL      Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
DR      EMBL: AB035140; BAA90296.1; -
DR      EMBL: AB035138; BAA90294.1; -
DR      EMBL: AB035139; BAA90295.1; -
DR      InterPro: IPR00478; -.
DR      Pfam: PF00229; TNF_1.
DR      PRINTS: PR01234; TNECROSISFCT.
DR      PROSITE: PS00251; TNF_1.
DR      PROSITE: PS0049; TNF_2.
SQ      SEQUENCE 280 AA; 31367 MW; F0E284D61A132EB4 CRC64;

```

Query Match	18.4%;	Score 183;	DB 6;	Length 280;
Best Local Similarity	27.0%;	Pred. No. 1.3e-08;		
Matches	50;	Conservative	38;	Mismatches 73; Indels 24; Gaps 6;
OY	5	TSEETITPTVOEQKQONISPLVRERCFORVAHNTTGRGNSNTLSSPNSKKEKALGRKNSM	64	
DB	117	TSQKHTTASLEQIGHPSPEPEKKQRYAHLTG-----KPKSRMPL-----EW	161	
OY	65	ESSRSQSHSLNHLNKGELVIERKEFYIYSQTYFRQOEIKENTKNDQWQYIY-KY	123	
DB	162	EDT-VGIYVLLSGVKKKKGGLVINEGLYVYSKYVFRQ-----SCTNLP.LSHKRYMKN	214	
OY	124	TSYPPPIILMKARRSCWCKDAEGLYSYIOGIGIFELKNDIIFYSYTNHILIDMDHES	183	
DB	215	SKYPPDVLMEGRKMS-YTTGQMANHSSYLDAVENLISADHLVYNSELSLVNEESOT	273	
OY	184	FFGAF	188	
DB	274	FFGLY	278	
RESULT	7			
ID	O9WV90	PRELIMINARY;	PRT;	169 AA.
AC	O9WV90;			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, last sequence update)		
DT	01-MAR-2001	(TREMBLrel. 16, last annotation update)		
DE	FAS LIGAND (FRAGMENT).			
OS	Marmota monax (woodchuck).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;			
OX	NCBI_Taxid=9995;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=HEALTHY LIVER;			
RA	Hodgson P.D., Grant M.D., Michalak T.I.;			
RT	"Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and			
RL	chronic woodchuck viral hepatitis.";			
CL	Cln. Exp. Immunol. 0:0-0(1999).			
EMBL	AF152368; AAD38387.1; -			
DR	InterPro; IPR000478; -			
DR	Pfam; PF00229; TNF; 1.			
DR	PROSITE; PS00251; TNF_1; 1.			
DR	PROSITE; PS0049; TNF_2; 1.			
DR	SMART; SM00207; TNF; 1.			
FT	NON_TER	1		
FT	NON_TER	1		
FT	NON_TER	169		
FT	NON_TER	169		
SEQUENCE	169 AA;	19274 MW;	FDE395B014717B6B	CRC64;
Query Match	17.3%;	Score 172;	DB 11;	Length 169;
Best Local Similarity	28.4%;	Pred. No. 6.5e-08;		
Matches	52;	Conservative	35;	Mismatches 56; Indels 40; Gaps 9;

OY		4	R	TSEETITVQKQKQONISPLVERPQPRAAAITGRRSNTLSPNSKNEKALGRKINS	63
Db		18	R	NTEETSL-----EKQIGHPSPSDKALKLRRAHLT---GKNRNRSSP-----LE	58
OY		64	W	ESSRSRGSHLSNLHRLNGELVIHERGFYYIYSQTYPFRFOEIKENTKNDKOMVOYTY-K	122
Db		59	W	EET- YGISLLISGVAYOKGGLAVINDTGLEYFSKYTIFFRQO-----SCNNPLSHRYVK	111
OY		123	Y	TSYSDPDILLMK-SARNSC-----SKDAEVLVLYSGIGIELEKENDIIFVSYNHELI	176
Db		112	N	SKYPODVLVMEGKKMMNCTTGOMMAR-----SSYLGAVERNFTSNIDLHYVNSELSLI	164
OY		177	D	MED 179	
Db		165	N	FEE 167	
RESULT		8			
O918D8			P	RELIMINARY;	272 AA.
AC	O918D8:				
DT	01-OCT-2000 (TREMBLrel. 15	Created)			
DT	01-OCT-2000 (TREMBLrel. 15,	Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16,	Last annotation update)			
DE	POTATIVE CD154 (CD40 LIGAND).				
GN	CD154.				
OS	Gallus gallus (Chicken).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
CC	Gallus.				
OX	NCBI_TaxID=9031;				
RP	[1]				
RN	SEQUENCE FROM N.A.				
RC	STRAIN-WHITE LECHORN LINE 0; TISSUE-SPLEEN;				
RA	Tregaskes C.A., Young J.R., Burnside J.				
RT	"Cloning of a putative chicken Cd40 ligand."				
.RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.				
DR	EMBL, AJ243435; CAB95748.1; "				
DR	InterPro: IPR000478; "				
DR	Pfam: PF00229; TNF_1.				
DR	PROSITE: PS00251; TNF_1; 1.				
DR	PROSITE: PS00409; TNF_2; 1.				
SO	SEQUENCE 272 AA; 30862 MW; 5409F24ABE53CDD7 CRC64;				

[illegible]

DE VASCULAR ENDOTHELIAL CELL GROWTH INHIBITOR.
GN VEGI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=VASCULAR ENDOTHELIAL;
RA Yu G.-L., Zhai Y., Ni J., Irueala-Arispe L., Huang W.-Q., Xing L.,
RA Lu J., Kozak D., Jiang G.-W., Rojas L., Janat M.F., Buengin M.,
RA Gertz R., Lippman M.E., Aggarwal B.B., Ruben S., Gertz R., Li L.-Y.,
RA Yu G.-L.;
RT "A Novel Endothelial Cell-Specific Negative Regulator of
RT Angiogenesis.";
RT Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL, AF039390, AAD08783.1; -.
DR HSSP, P01375; ATSV.
DR InterPro, IPR000478; -.
DR InterPro, IPR003636; -.
DR Pfam, PF00229; TNF_1.
DR PRINTS, P01234; TNECROSISFCF.
DR PRODOM, PD002012; -; 1.
DR PROSITE, PS00049; TNF_2; 1.
DR SMART, SM00207; TNF_1.
SQ SEQUENCE 174 AA; 20131 MW; CCB83BA7EE673B98 CRC64;

[illegible]

[3]
 RN SEQUENCE FROM N.A.
 RC TISSUE-LYMPHOMA:
 RA Force W.R., Todd P.K., Mikayama T.;
 RT "Mouse Lymph: Molecular Genetics, Ligand Binding and Expression";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB029155; BAA8559.1; -
 DR EMBL: AF123385; AAF76453.1; -
 DR EMBL: AF227533; AAF36722.1; -
 DR HSSP: P01375; 4TSV.
 DR InterPro: IPR000478; -
 DR Pfam: PF00229; TNE; 1.
 DR PRINTS: PR01234; TNECROSISFCT.
 DR PROSITE: PS00049; TNE_2; 1.
 SQ SEQUENCE 239 AA; 26338 MW; 217874AC71AD6B83 CRC64;

Query Match 15.3%; Score 152.5; DB 11; Length 239;
 Best Local Similarity 29.2%; Pred. No. 5.4e-06;
 Matches 47; Conservative 25; Mismatches 72; Indels 17; Gaps 6;
 QY 33 AAHTTGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLMLHNLNGELVTHEKGFY 92
 DB 93 AAHLTGANASLIGIGP-----LIME-TRIGLAFRLGLTYHDGLVTMEPGY 139
 QY 93 YIYQTYFRQEEIKENTKNDKQWYIYKYTS-YPPDILKSGARNSCWSKDAEYGLY- 150
 DB 140 YVYSKVOLS-GVCCPQGLANGLPITTHGLYKRTSRYPKELELVRSRSCGANSRRVWMD 198
 QY 151 SIYOGIFELKENDRIFVSTNEHLI-DMDEASFGCAFVY 190
 DB 199 SSFLGVHLEAGEEYVVRPGNRLVPRGRTSRYFCAFVY 239

RESULT 11
 070332 ID 070332 PRELIMINARY; PRT; 216 AA.
 AC 070332;
 DT 01-AUG-1998 (Tremblrel. 07, Created)
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
 DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE TUMOR NECROSIS FACTOR-ALPHA (FRAGMENT).
 OS Mesocricetus auratus (Golden hamster).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 NCBI_TaxID=10036;
 RX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SPLEEN;
 RA MEDLINE=98234044; PubMed=9573100;
 RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
 RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
 RT analysis of cytokine mRNA expression in experimental visceral
 RT leishmaniasis";
 RL Infect. Immun. 66:2135-2142(1998).
 DR EMBL: AF046215; AAC40100.1; -
 DR HSSP: P06804; 2TNE.
 DR InterPro: IPR000478; -
 DR Pfam: PF00229; TNE; 1.
 DR PRINTS: PR01234; TNECROSISFCT.
 DR PROSITE: PS00251; TNE_1; 1.
 DR PROSITE: PS00049; TNE_2; 1.
 DR SMART: SM00207; TNE; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 216 AA; 23793 MW; BADAE3F83F45B533 CRC64;

Query Match 14.5%; Score 144.5; DB 11; Length 216;
 Best Local Similarity 26.9%; Pred. No. 2.4e-05;
 Matches 47; Conservative 28; Mismatches 63; Indels 37; Gaps 7;

QY 28 GPORYAAH---ITGTRGRSNTL-SSPNSKNEKALGRKINS-----MESSRSGHSFLS 75
 DB 49 GPORBEKFPNPIITSGTGTLTRSSONSNDKPVGHVYVANHQVDEQLMLSHRAALLN 108
 QY 76 NLHLRNGELVTHEKGFYIYQTYFRQEEIKENTKNDKQWYIYK-----YTSYPD 128
 DB 109 GMSLKNDQVLIPADGLVLYSQVLEFRG-----GCPSYVLTHTVSRIAYSVED 157
 QY 129 PILKKSARNCSKSDAEYG-----LSTIYOGIFELKENDRIFVSTNEHLID 177
 DB 158 NVNLLSAIKSPC-PKETPEGELKPMYEPYILGVGFQLEKGDRLSAEYVNLPRYLD 211

RESULT 12
 09ERG6 ID 09ERG6 PRELIMINARY; PRT; 217 AA.
 AC 09ERG6;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE TUMOR NECROSIS FACTOR ALPHA (FRAGMENT).
 OS Peromyscus maniculatus (Deer mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 OC Peromyscus.
 NCBI_TaxID=10042;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SPLEEN;
 RA Herbst M.M., Schountz T.;
 RT "Cloning of the deer mouse interferon gamma, interleukin-10 and tumor
 RT necrosis factor genes";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF307013; AAG30264.1; -
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 217 AA; 23964 MW; D6F90C74C0B3021F CRC64;

Query Match 13.6%; Score 135; DB 11; Length 217;
 Best Local Similarity 24.7%; Pred. No. 0.00017;
 Matches 43; Conservative 35; Mismatches 72; Indels 24; Gaps 7;
 QY 20 ISPLVBERGPPVAAHTIGTRGRSNTL-SSPNSKNEKALGRKINS-----MESSRSG 70
 DB 48 IGPORBEKFPNPLP--ILGSAQITLTKRSSQSSDKPVAVVANHQVDEQLMLSHRAAN 105
 QY 71 HSPFLNHLRNGELVTHEKGFYIYQTYFRQEEIKENTKNDKQWYIYK-TSYPDP 129
 DB 106 ALLANGMDLKNOLVLPADGLVLYSQVLEFRG-----GCSNYVLTHTVSRIAYSVEDK 160
 QY 130 ILLKKSARNCSKSDAEYG-----LSTIYOGIFELKENDRIFVSTNEHLID 177
 DB 161 VNLLSAIKSPC-PKETPEGSELKPMYEPYILGVGFQLEKGDRLSAEYVNLPRYLD 213

RESULT 13
 035853 ID 035853 PRELIMINARY; PRT; 232 AA.
 AC 035853;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE TUMOR NECROSIS FACTOR ALPHA.
 GN TNFA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A/J;
 RX MEDLINE=97246744; PubMed=9089109;

RA Iraqi F., Teale A.;
RT Cloning and sequencing of the tufa genes of three inbred mouse
strains.";
RL Immunogenetics 45:459-461(1997).
DR EMBL: U68414; AAB5593.1; -.
DR HSSP: P06804; 2TNF.
DR InterPro: IPR000478; -.
DR InterPro: IPR003636; -.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR PRODOM: PD002012; -. 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR SMART: SM00207; TNF; 1.
SQ SEQUENCE 232 AA; 25513 MW; 2ED6DA8E0DCAADD8 CRC64;

Query Match 13.2%; Score 131.5; DB 11; Length 232;
Best Local Similarity 23.0%; Pred. No. 0.00038;
Matches 41; Conservative 35; Mismatches 77; Indels 25; Gaps 7;

QY 28 GPOVAHAHTG---TRGRSNTLSSPNSKNEKALGRKINS-----WESSRSGHSFLSN 76
DB 57 GPORDEKFPNGLLISMAQTLSOSSSDKPYAHVANHQVEQLEMLSQANALLANG 116
QY 77 LHLNGELVIHEKGYIYSQYFRFOEIKENTKNDKQNVQYIKYT-SYPPITLMS 135
DB 117 MDKMDQLVVPADGLVYSQVLEKQ-----GCPDYVLLTHVSRPAISYQEKVNLLSA 171
QY 136 ARSCMSKDAEYG-----LYSIQGIIFELKENDRFVSVTEHLDMHKS-FPG 186
DB 172 VKSPC-PKDPPEGAELKPWEPIYLGVFQLEKGDLSAEVNLPKYLDFAESGOVYFG 228

RESULT 14

Q91B42 PRELIMINARY; PRT; 225 AA.

AC Q91B42;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE TUMOR NECROSIS FACTOR.
OS Paratichthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygii; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Bothidae; Paralicthys.
OX NCBI_Taxid=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Hiroo I., Nam B., Kurabe T., Aoki T.;
RT "Molecular cloning, characterization and expression of tumor necrosis
factor (TNF) cDNA and gene from Japanese flounder Paralicthys
RT olivaceus";
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: A040448; BAA94969.1; -.
DR InterPro: IPR000478; -.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR PROSITE: PS50049; TNF_2; 1.
SQ SEQUENCE 225 AA; 24965 MW; 8F947FB25FC82658 CRC64;

Query Match 12.7%; Score 126.5; DB 13; Length 225;
Best Local Similarity 22.0%; Pred. No. 0.001;
Matches 42; Conservative 40; Mismatches 78; Indels 31; Gaps 8;

QY 15 EKOQNTSPLVREGPQVAHAHTGTRGRSNTLSSPNS--KNKALGRKINSWESSRSGH 71
DB 47 EKTEPHNTLRQISRAKAALHLEG-RDEDEETSENKLVKKNDEGLA-----FTGGGF 98
QY 72 SFLSNLHNGELVIHEKGYIYSQYFRFO-----EIKENTKNDKQNVQY-IKYT 124

DB 99 ELVDN-----HIIIPRGLIYVYQASFRVSCSSDDADGKEAERKHLTISHRWLEF 152
QY 125 -SYDPDILLKMSARNSCWS-----KDAEYGLYSIYQGIIFELKENDRIFVSVTNEHLID 177
DB 153 ESLGTQVSLMSAVRSACQKQEDAYRQCGWYNAITYGAFQLENGKMTETINMLSELE 212
QY 178 MDHEASFFGAF 188
DB 213 TESGKTEFGVF 223

RESULT 15

Q9UKS8 PRELIMINARY; PRT; 205 AA.

AC Q9UKS8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE LYMPHOTOXIN ALPHA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,
RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,
RA Lasky S., Hood L.;
RT "Sequence of the human major histocompatibility complex class III
region.";
RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF129756; AAD18092.1; -.
DR HSSP: P01375; 4TSV.
DR InterPro: IPR000478; -.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR SMART: SM00207; TNF; 1.
FT VARIANT 1 M -> L.
SQ SEQUENCE 205 AA; 22310 MW; BA0C25B7930A3A92 CRC64;

Query Match 12.3%; Score 122.5; DB 4; Length 205;
Best Local Similarity 22.5%; Pred. No. 0.0021;
Matches 43; Conservative 31; Mismatches 78; Indels 39; Gaps 7;

QY 9 TISTVDEKQ-----NISPLVREGRQVAHAHTGTRGRSNTLSSPNSKNEKALGR 59
DB 41 TPSAQTARQHPKMHLSNMLKP-----AAHLIGDPSKQNSL----- 77
QY 60 KISMWESSRSGHSFLSNLHNGELVIHEKGYIYSQYFRFOEIKENTKNDKQNVQY 119
DB 78 --LWRANDRAFLQDGFSLSNSLVLPTGILFYVSQVYFSKAKSPKATSSPLYLAHE 134
QY 120 IYKVT-SYDPDILLKMSARNSCWSKDAEGLYSIYQGIIFELKENDRIFVSVTNEHLID 177
DB 135 VOLFSSQYFPHVPL-LSSQKMYVPGIQLPEWLSHMYGAFAFOLTGQDOLSTHTDGIPHLV- 192
QY 178 MDHEASFFGAF 188
DB 193 LSPSTVFFGAF 203

Search completed: October 1, 2001, 11:44:23
Job time: 109 sec

A;Molecule type: mRNA
A;Residues: 1-281 <RES>

[illegible]

	Query Match	17.8%	Score 177.5	DB 2	Length 278:
	Best Local Similarity	27.5%	Pred. No. 2,2e+08:		
	Matches	50;	Conservative 39;	Mismatches 64;	Indels 29; Gaps 8
OY	10 ISTVQKQONISPLVERGPGPQRYAAHITCT--RGRSNTLSSPSNKEKALGRKINSMESSR	68			
Db	121 VSSFQKOINLPSTPEETKKPRSV-AHLTGNNPRSRSIPL-----EWEEDT-	162			
OY	69 SCHSFSLNLHNGELVIHEKGFIYYISOTYRRFOEIKENTKNDKOMQYIY-KYTSP	127			
Db	163 YCTALISGKYKKRGGLGVINEAGLIIVYSKVYIRGQ-----SCNSDPLSHKYYMRNFKP	216			
OY	128 DPLIMKSAR-NSCSKDQAEYGLSYIOGIFELKENDRIEVSVTNEHLIDMDHEADSPFG	186			
Db	217 GDVLIMEEKILNYCTT--GIWIAHSSYLGAVERNLTIVADLVYNISOLSLINEESKTFFPG	274			
OY	187 AF 188				
Db	275 LV 276				

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RESULT      4
S53090
CD40_ligand - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C:Accession: S53090
R:Mertens, B.E.L.C.; Muriuki, M.
Submitted to the EMBL Data Library, February 1995
A:Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A:Reference number: S53090
A:Accession: S53090
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-261 <MEK>
A:Cross-references: EMBL:Z48469; NID:g732569; PIDN:CAA88363.1; PID:g732570

Query Match          14.3%; Score 142; DB 2; Length 261;
Best Local Similarity 27.7%; Pred. NO.2.9e+05;
Matches    49; Conservative   33; Mismatches   69; Indels   26; Gaps     8
```

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RESULT      5
S17289
tumor necrosis factor beta precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S17289
R:Kunert, P.; Wuehrlich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A:Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative a
A:Reference number: S17289; MUID:91340150
A:Accession: S17289
A:Molecule type: DNA
A:Residues: 1-204 <KJH>
A:Cross-references: EMBL:X54859; NID:92132; PIDN:CA38638.1; PID:g2133
C:Genetics:
A:Introns: 32/3; 68/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage

```


Db 124 VFPDGLYLIVSOVLFFGQGCPTNWFTHHTISRIA-----VSOTKVLMSAIKSPQ 177
 QY 142 SK-----DAEYGLYSYOGGIFELKENDRIFFSVTNEHLIDMDHEAS-FFG 186
 Db 178 REPPEGAEAPWYEPITLGGVFOLEKDRLSAEINLPDIYDFAEASGVYFG 228

RESULT 8

154490

tumor necrosis factor alpha precursor - white-footed mouse

C:Species: Peromyscus leucopus (white-footed mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000

C:Accession: I54490

R:Crew, M.D.; Filipowsky, M.E.

Immunogenetics 35, 351-353, 1992

A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leuc

A:Reference number: I54490, M0ID:92218012

A:Accession: I54490

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-235 <RES>

A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA0596.1; PID:g202507

C:Genetics:

A:Gene: pTNF

A:Introns: 62/3; 81/1; 97/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation

F:19/20/Binding site: myristate (Lys) (covalent) #status predicted

F:84/Binding site: carboxydrate (Ser) (covalent) #status predicted

Query Match

Best Local Similarity 13.0%; Score 129.5; DB 2; Length 235;

Matches 45; Conservative 39; Mismatches 75; Indels 25; Gaps 9;

QY 20 ISPLVERGQRAAHHTGRGSRNLT-SSPNKNEKALRKINSMP-----SSSGH 71

Db 56 IGQREKKEFPNNLP--TIGSMAQTTLTRSSSSQSDKPAHVAVAHQVDOLEMLSGAN 113

QY 72 SFLSN-LHLNGLVLIHEKGFYIYSOTYFRFOEIKENKNDKQMYIYK-TSPDP 129

Db 114 ALLANGLMDKNDLVIPADDLIVISQVLFKQ-----GSSVYLTHIYSRPAVSIEDK 168

QY 130 ILLKKSARNSCSKDAEYG-----LYSIYOGGIFELKENDRIFFSVTNEHLIDMDHEAS 183

Db 169 VNLISAIKSPC-FKPEPEGSELKPWYEPITLGGVFOLEKDRLSAEVNLPRKYLDFAESG 227

QY 184 -FFG 186

Db 228 VYFG 231

RESULT 9

S21738

CD40 ligand - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999

C:Accession: S21738

R:Armstrong, R.J.; Fanslow, W.C.; Strockbine, L.; Sato, T.A.; Clifford, K.N.; Macduff, B.

Nature 357, 80-82, 1992

A:Title: Molecular and biological characterization of a murine ligand for CD40.

A:Reference number: S21738; M0ID:92244364

A:Accession: S21738

A:Molecule type: mRNA

A:Residues: 1-260 <ARM>

A:Cross-references: EMBL:X65453; NID:g50351; PIDN:CAA46448.1; PID:g50352

C:Keywords: glycoprotein; transmembrane protein

F:23-46/Domain: transmembrane #status predicted <TM>

F:47-260/Domain: extracellular #status predicted <EXT>

F:239/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 12.8%; Score 127.5; DB 1; Length 204;

Matches 47; Conservative 29; Mismatches 78; Indels 35; Gaps 9;

QY 9 TISTVGEKQONISPLVREKGPQVAAHITG-----TRKSTLSPNKNKALGRKI 61

Db 40 TPSAAPAHQOL-PTPTRTGLKPAHLVGDPSQSLMRANT-----DRAFLR-- 88

QY 62 NSMESSRSGHSLNHLRNGELVIEHKGFIYSOTYFRFOEIKENKNDKQMYIY 121

Db 89 -----HGF-----SLSNSILVPTSGLYFYSSQVVFSGRCFPRAFTPTPLIAHEVQ 135

QY 122 KYT-STYDPIILKKSARNSCSKDAEYGLYSYOGGIFELKENDRIFFSVTN- EHLIDMD 179

Db 136 LFSPOYFHVPLLSAQKSVCPGPGPW-VRSVYQAVFLLTRDQSLSTHIDGISHL-LS 193

QY 180 HEASFGAF 188

Db 194 PSSVFGAF 202

RESULT 11

JQ1344

tumor necrosis factor alpha precursor - horse

N:Alternate names: cachectin; TNF alpha

C:Species: Equus caballus (domestic horse)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C:Accession: JQ1344

R:Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosi

A:Reference number: JQ1344; M0ID:92084125

A:Accession: JQ1344

A:Molecule type: DNA

A:Residues: 1-234 <SU>

A:Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245

Query Match 12.9%; Score 128.5; DB 2; Length 260;
 Best Local Similarity 25.3%; Pred. No. 0.00046;
 Matches 44; Conservative 35; Mismatches 68; Indels 27; Gaps 8;

QY 4 RTSEFTISY-----QEQONISPLVREKGPQVAAHITGTRGSRNLTSSPNKNEKALGR 59

Db 89 RQEDLVKDTTLNKEEKENSFEMQGDDEPQIAAHV-----VSEANSMAAYL-- 137

QY 60 KINSMESSRSGHSLNL-FLRNG-ELVIEHKGFIYSOTYFRFOEIKENKNDKQMY 117

Db 138 ---QW-AKKQYITMKSMLVNLKNGKQLTVRREGIYYTYVTCNSNE-----PSSQRPFI 189

QY 118 QYIKYTSYDPIILKKSARNSCSKDAEYGLYSYOGGIFELKENDRIFFSVT 171

Db 190 VGLMKPISGSEIRILKKAANTHSSQICEQ--QSVHLGVEFELQAGASVFNVT 241

RESULT 10

S24641

lymphotoxin - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: I46046; S24641

R:Cludts, T.; Cleuter, Y.; Kettmann, R.; Burry, A.; Droogmans, L.

Cytokine 5, 336-341, 1993

A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and

A:Reference number: I46046; M0ID:94083525

A:Accession: I46046

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-204 <CL2>

A:Cross-references: EMBL:214137; NID:g796; PIDN:CAA78510.1; PID:g797

C:Genetics:

A:Introns: 32/3; 68/1

C:Superfamily: tumor necrosis factor

Query Match

Best Local Similarity 12.8%; Score 127.5; DB 1; Length 204;

Matches 47; Conservative 29; Mismatches 78; Indels 35; Gaps 9;

QY 9 TISTVGEKQONISPLVREKGPQVAAHITG-----TRKSTLSPNKNKALGRKI 61

Db 40 TPSAAPAHQOL-PTPTRTGLKPAHLVGDPSQSLMRANT-----DRAFLR-- 88

QY 62 NSMESSRSGHSLNHLRNGELVIEHKGFIYSOTYFRFOEIKENKNDKQMYIY 121

Db 89 -----HGF-----SLSNSILVPTSGLYFYSSQVVFSGRCFPRAFTPTPLIAHEVQ 135

QY 122 KYT-STYDPIILKKSARNSCSKDAEYGLYSYOGGIFELKENDRIFFSVTN- EHLIDMD 179

Db 136 LFSPOYFHVPLLSAQKSVCPGPGPW-VRSVYQAVFLLTRDQSLSTHIDGISHL-LS 193

QY 180 HEASFGAF 188

Db 194 PSSVFGAF 202

J.R. Kobayashi, Y.; Miyamoto, D.; Asada, M.; Ohinata, M.; Osawa, T.
 J. Biochem. 100, 727-733, 1986
 A.Title: Cloning and expression of human lymphotoxin mRNA derived from a human T cell by
 A.Reference number: A91906; MUID:8705135
 A.Accession: A91906
 A.Molecule type: mRNA
 A.Residues: 1-59, 'N', '61-205 <KOB>
 A.Cross-references: GB:000102; NID:g219913; PIDN:BA00064.1; PID:g219914
 A.Note: the authors translated the codon TAT for residue 156 as Thr and ACC for residue
 R:Rukuda, S.; Ando, S.; Sanou, O.; Taniat, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An
 Lymphokine Res. 7, 175-185, 1988
 A.Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
 A.Reference number: A61478; MUID:88301617
 A.Accession: A61478
 A.Molecule type: protein
 A.Residues: 56-79;86-95, 'X', 97, 'X', 99,119-151, 'XX',154-162, 'X',164, 'X',166, 'X',168, 'X',1
 R:Voigt, C.G.; Maurer-Fogy, I.; Adolff, G.R.
 FEBS Lett. 314, 85-88, 1992
 A.Title: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosylation
 A.Reference number: S26951; MUID:93083656
 A.Accession: S26951
 A.Molecule type: protein
 A.Residues: 35-59, 'N', '61-205 <VOI>
 A.Note: 60-Thr was also found
 R:Fukushima, K.; Watanabe, H.; Takeo, K.; Nomura, M.; Asahi, T.; Yamashita, K.
 Arch. Biochem. Biophys. 304, 144-153, 1993
 A.Title: N-linked sugar chain structure of recombinant human lymphotoxin produced by CHO
 A.Reference number: S34742; MUID:93311995
 A.Contents: annotation
 C:Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after induction,
 while having no detrimental effect on normal cells. It can also act synergistically with
 C:Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of differ
 ical activities but are produced by different cell types and have different induction ki
 C:Genetics:
 A:Gene: GDB:LTA; LT; TNFB
 A:Cross-references: GDB:120442; OMIM:153440
 A:Map position: 6p21.3-6p21.3
 A:Introns: 33/3; 69/1
 A>Note: the first intron occurs before the initiator codon
 C:Summary: tumor necrosis factor
 C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lymphokine; macrophage
 F:1-34/Domain: signal sequence #status predicted <SIG>
 F:35-205/Product: lymphotoxin #status predicted <MNT>
 F:41/Binding site: carbohydrate (Thr) (covalent) #status experimental
 F:96/Binding site: carbohydrate (Asn) (covalent) #status experimental

A>Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis factor
A:Reference number: A22908; MUID:88224564
A:Accession: A22908
A:Molecule type: DNA
A:Residues: 1-235 <SH>
A:Cross-references: GB:M20155
R:Shakhov, A.N.; Nedospasov, S.A.
Bioorg. Khim. 13, 701-705, 1987
A>Title: Molecular cloning of the genes coding for tumor necrosis factors: complete n
A:Reference number: 503791; MUID:87296639
A:Accession: 503791
A:Molecule type: DNA
A:Residues: 1-235 <SHA>
A:Cross-references: GB:M8296; NID:g202086; PIDN:AAA40459.1; PID:g202087
A>Note: article in Russian with English abstract
R:Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
A>Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor
A:Reference number: A93679; MUID:88067722
A:Accession: A27303
A:Molecule type: DNA
A:Residues: 1-235 <SEN>
A:Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID:g54832
R:Pemilia, D.; Hayflick, J.S.; Bringham, T.S.; Palladino, M.A.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985
A>Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necr
A:Reference number: A25164; MUID:85298296
A:Accession: A25164
A:Molecule type: mRNA
A:Residues: 1-235 <PEN>
A:Cross-references: GB:M1731; NID:g202084; PIDN:AAA40458.1; PID:g202085
R:Fransen, L.; Muller, R.; Marmonout, A.; Tavernier, J.; van der Heyden, J.; Kawashim
Nucleic Acids Res. 13, 4417-4429, 1985
A>Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic ex
A:Reference number: A23127; MUID:85242112
A:Accession: A23127
A:Molecule type: mRNA
A:Residues: 1-235 <PRA>
A:Cross-references: GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g54845
R:Chen, K.; Beutler, B.
J. Biol. Chem. 264, 16256-16260, 1989
A>Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide resul
A:Reference number: A34251; MUID:89380231
A:Accession: A34251
A:Molecule type: protein
A:Residues: 70-87 <CSE>
A:Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shiner, S.L.; Cerami, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A>Title: Identification of a common nucleotide sequence in the 3'-untranslated region
A:Reference number: I59058; MUID:66149365
A:Accession: I59058
A>Status: preliminary; translated from GE/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-230/'R', 232-235 <RES>
A:Cross-references: GB:M3049; NID:g202082; PIDN:AAA40457.1; PID:g202083
R:Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990
A>Title: Characterization of high molecular weight glycosylated forms of murine tumor
A:Reference number: A36696; MUID:91097531
A:Accession: A36696
A:Molecule type: protein
A:Residues: 80-85,'X',87-99 <SHE>
C:Genetics:
A:introns: 62/3; 81/1; 97/1
A>Note: The first intron occurs in the 5'-untranslated region
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
E:80-235/Product: tumor necrosis factor #status experimental <MAT>
F:20/Binding site: myristate (Lys) (covalent) #status predicted
F:84/Binding site: carboxydrate (Ser) (covalent) #status predicted
F:86/Binding site: carboxydrate (Asn) (covalent) #status predicted
F:148-179/Dissulfide bonds: #status predicted

